

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 15, 2005, 09:15:21 ; Search time 6503.04 Seconds
(without alignments)
10141.035 Million cell updates/sec

Title: US-09-922-067F-9
Perfect score: 1361
Sequence: 1 tggagactaagctgaaact.....agggaatagagaatacaatt 1361

Scoring table:
IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*
1: gb.ba.*
2: gb.htg.*
3: gb.in.*
4: gb.on.*
5: gb.ov.*
6: gb.pat.*
7: gb.ph.*
8: gb.pl.*
9: gb.pr.*
10: gb.ro.*
11: gb.sts.*
12: gb.sy.*
13: gb.un.*
14: gb.vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1361	100.0	1361	6	A41956 Sequence 9
2	1361	100.0	1361	6	AR080658 Sequence
3	1361	100.0	1361	6	AR084987 Sequence
4	1361	100.0	1361	6	AR125358 Sequence
5	1361	100.0	1361	6	BD242703 Method fo
6	1361	100.0	1361	6	AR205614 Sequence
7	1361	100.0	1361	6	AX006795 Sequence
8	1361	100.0	1561	6	AX335487 Sequence
9	1361	100.0	1561	9	HSU24577
10	1359.4	99.9	1505	6	CO717247 Sequence
11	1359.4	99.9	1505	9	HSU20157
12	1359.4	99.9	1520	6	AR13777 Sequence 7
13	1359.4	99.9	1520	6	AR064404
14	1359.4	99.9	1520	6	AR083755 Sequence
15	1359.4	99.9	1520	6	AR141150 Sequence
16	1359.4	99.9	1520	6	AR142503 Sequence
17	1359.4	99.9	1520	6	I23385 Sequence 7
18	1359.4	99.9	1520	6	I49901 Sequence 7
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ALIGNMENTS

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LOCUS A41956 1361 bp DNA linear PAT 05-MAR-1997
DEFINITION Sequence 9 from Patent WO9500649.
ACCESSION A41956
VERSION A41956.1 GI:2297493
KEYWORDS
SOURCE unidentified
ORGANISM unclassified
REFERENCE 1 (bases 1 to 1361)
AUTHORS Macphree,C.H., Tew,D.G., Southan,C.D., Hickey,D.M., Gloger,I.S., Lawrence,G.M. and Rice,S.Q.
TITLE LIPOPROTEIN ASSOCIATED PHOSPHOLIPASE A 2?, INHIBITORS THEREOF AND USE OF THE SAME IN DIAGNOSIS AND THERAPY
JOURNAL Patent: WO 9500649-A 9 05-JAN-1995;
SMITHKLINE BEECHAM PLC (GB)
COMMENT Other publication JP 8500740T 960130.
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Query Match 100.0%; Score 1361; DB 6; Length 1361;
Best Local Similarity 100.0%; Pred. No. 0;
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RESULT 3
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DEFINITION Sequence 9 from patent US 5981252.
ACCESSION AR084987
VERSION AR084987.1 GI:10011758
KEYWORDS Unknown.

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ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1361)  
AUTHORS MacPhee, C. Houston, and Tew, D. Graham.  
TITLE Lipoprotein associated phospholipase A.sub.2, inhibitors thereof  
and use of the same in diagnosis and therapy  
JOURNAL Patent: US 5981252-A 9 09-NOV-1999;  
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Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1361; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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Db 1 TGAGAGACTAGCTGAAACTGCTGCTCAGCTCCCAAGATGCTGCCACCAAAATTCGATGT 60  
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LOCUS AR205614 1361 bp DNA linear PAT 20-JUN-2002
DEFINITION Sequence 9 from patent US 6369045.
ACCESSION AR205614
VERSION AR205614.1 GI:21503242
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 1361)
Macphree,C.Houston., Tew,D.Graham. and Hickey,D.Mary.Bernadette.
Phospholipase A2 inhibitors thereof and use of same in diagnosis
and therapy
JOURNAL Patent: US 6369045-A 9 09-APR-2002;
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ACCESSION AX006795
VERSION AX006795.1 GI:9994827
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
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Gloger,I.S., Hickey,D.M., Macphree,C.H., Southan,C.D.,
Lawrence,G.M., Rice,S.Q. and Tew,D.G.
Lipoprotein associated phospholipase a2, inhibitors thereof and use
of same in diagnosis and therapy
JOURNAL Patent: EP 0974663-A 9 26-JAN-2000;
SMITHKLINE BEECHAM PLC (GB)
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HSU24577
LOCUS Human LDL-phospholipase A2 mRNA linear PRI 24-JUL-1996
DEFINITION Human LDL-phospholipase A2 mRNA, complete cds.
ACCESSION U24577
VERSION U24577.1 GI:1314245
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1561)
Tew, D.G., Southan, C., Rice, S.Q., Lawrence, M.P., Li, H., Boyd, H.F.,
Moore, K., Gloger, I.S. and Macpherson, C.H.
Lipoprotein-associated, serine-dependent phospholipase involved in
the oxidative modification of low-density lipoproteins
Arterioscler. Thromb. Vasc. Biol. 16 (4), 591-599 (1996)
JOURNAL 96197208
MEDLINE 8624782
PUBMED
REFERENCE 2 (bases 1 to 1561)
Rice, S.Q.J.
Direct Submission
Submitted (10-APR-1995) Simon Q.J. Rice, SmithKline Beecham
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Harlow, Essex CM195AW, UK
COMMENT On May 16, 1996 this sequence version replaced gi:790655.
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VERSION CQ717247.1 GI:42278104
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
TITLE Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
thereof
JOURNAL Patent: WO 02068579-A 3181 06-SEP-2002;
PS Corporation
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ACCESSION U20157
VERSION U20157.1 GI:780132
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REFERENCE 1 (bases 1 to 1505)
AUTHORS Tjoelker L.W., Wilder, C., Eberhardt C., Stafforini, D.M., Ditsch, G., Schimpf, B., Hooper, S., Trong, H., Cousens, L.S., Zimmerman, G.A., Yamada, Y., McIntyre, F.M., Prescott, S.M. and

Gray, P.W.
Anti-inflammatory properties of a platelet-activating factor acetylhydrolase
Nature 374 (5522), 549-553 (1995)
95214779
PUBMED 7700381
AUTHORS Tjoelker, L.W.
TITLE Direct Submission
JOURNAL Submitted (20-JAN-1995) Larry W. Tjoelker, ICOS Corporation, 22021 20th Ave. S.E., Bothell, WA 98021, USA
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VERSION A81377.1 GI:6731692
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REFERENCE 1 (bases 1 to 1520)
AUTHORS Eberhardt,C.D. and Gray,P.
TITLE TRUNCATED PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE

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Best Local Similarity 99.9%; Pred No. 0;
Matches 1360; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 TGAGAGACTAAGCTGAACTGCTCAGCTCCCAAGATGGTGCACCCAAATTCATGT 60
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GenCore version 5.1.6
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5	1359.4	99.9	1505	11	ADP64943 Human pho
6	1359.4	99.9	1505	11	ADP65357 Human pla
7	1359.4	99.9	1505	12	ADH43822 Human pla
8	1359.4	99.9	1505	12	ADJ74586 Human pla
9	1359.4	99.9	1505	12	ADP12846 Reference
10	1359.4	99.9	1505	13	ADR25259 Breast ca
11	1359.4	99.9	1505	13	ADR14276 Human NF-
12	1359.4	99.9	1505	13	ADP54610 Human PRO
13	1359.4	99.9	1505	13	ADP23966 PRO polyp
14	1359.4	99.9	1520	2	AAQ87947 Human pla
15	1359.4	99.9	1520	2	AAT80564 Human pla
16	1359.4	99.9	1520	2	AAT87048 Human pla
17	1359.4	99.9	1520	2	AAT96127 Human pla
18	1359.4	99.9	1520	2	AAX08463 Human pla
19	1359.4	99.9	1520	2	AAV08534 Human PAF
20	1359.4	99.9	1520	3	AA10861 Human pla

21	1359.4	99.9	1520	3	AAZ24240 Human PAF
22	1359.4	99.9	1520	3	AA59579 cDNA enco
23	1359.4	99.9	1520	4	AA04143 Human pla
24	1359.4	99.9	1520	4	AAAC89057 Platelet-
25	1359.4	99.9	1520	5	AA24719 Human pla
26	1359.4	99.9	1520	9	ADA19490 Human pla
27	1357.4	99.7	1520	2	AA63701 cDNA enco
28	1323	97.2	1323	6	AA036733 Human lip
29	1247.8	91.7	1320	4	AAAD04169 Mouse-Hum
30	1199.4	88.1	1203	10	ADG73659 Human PAF
31	1198.4	88.1	1563	10	ADG73667 Human hCB
32	1198.4	88.1	1917	10	ADG73669 Human gCB
33	1198.4	88.1	1929	10	ADG73671 Human gCB
34	1172.6	86.2	1320	4	AAAD04168 Mouse-Hum
35	1162.4	85.4	1335	2	AAAT87072 Human pla
36	1162.4	85.4	1335	3	AAA10885 Synthetic
37	1162.4	85.4	1335	3	AAZ24261 Human PAF
38	1162.4	85.4	1335	4	AA04165 Human pla
39	1162.4	85.4	1335	4	AAAC89078 Platelet-
40	1162.4	85.4	1335	5	AAAD24740 Human pla
41	1151.4	84.6	1336	9	ADA19513 cDNA rela
42	1049.6	77.1	1528	9	ADA19506 Cow plas
43	1049.6	77.1	1533	2	AAT87066 Bovine pl
44	1049.6	77.1	1533	2	AAX08478 Bovine pl
45	1049.6	77.1	1533	2	AAV08552 Bovine PA

ALIGNMENTS

RESULT 1

AAQ81780
ID AAQ81780 standard; cDNA; 1361 BP.

AC AAQ81780;
XX

DT 25-MAR-2003 (revised)
DT 18-AUG-1995 (first entry)

XX Human T-cell lymphoma lipoprotein-associated phospholipase-A2.

DE T-cell; T-lymphocyte; lipoprotein-associated phospholipase-A2; enzyme;
KW atherosclerosis; diagnosis; therapy; antiarteriosclerotic; ss.

OS Homo sapiens.

XX Key Location/Qualifiers

FT CDS 38..1357

FT /*tag= a

XX WO9500649-A1.

XX 05-JAN-1995.

XX 24-JUN-1994; 94WO-GB001374.

XX 25-JUN-1993; 93GB-00013144.

PR 11-JAN-1994; 94GB-00000413.

XX (SMIK) SMITHKLINE BEECHAM PLC.

XX Macphée CH, Tew DG, Southan CD, Hickey DMB, Gloger IS;

PI Lawrence GMP, Rice SQJ;

XX WPI; 1995-052086/07.

DR P-P5DB; AAR64928.

XX Purified lipoprotein associated phospholipase A2 - used to develop prods.

PT for diagnosis and therapy, partic. inhibitors for treatment of

XX atherosclerosis.

PS Claim 8; Page 19; 29pp; English.

XX Recombinant low density lipoprotein associated phospholipase A2, used to
 PT produce antibodies for diagnostics, is purified using a Blue Sepharose
 PT and Q Sepharose column.

PS Claim 6d; Page 15-17; 28pp; English.

XX The present sequence represents cDNA encoding human LDL-PLA2. The
 CC invention relates to a method for purifying recombinant low density
 CC lipoprotein-associated phospholipase A2 (LDL-PLA2). The method comprises
 CC applying a cell extract, supernatant or solution containing the
 CC recombinantly expressed LDL-PLA2 to a zinc chelating column, applying the
 CC eluate to a Blue Sepharose column, and applying that eluate to a Q
 CC Sepharose column. The invention also provides a process which
 CC additionally comprises the prior steps of constructing a vector
 CC comprising a cDNA encoding a histidine tagged LDL-PLA2 or fragment
 CC thereof, expressing the tagged protein in a host cell, isolating the
 CC tagged protein from the harvest medium or cell lysate, purifying the
 CC protein using a metal matrix affinity column (preferably a nickel
 CC column), and removing the histidine tag by protease cleavage. LDL-PLA2,
 CC also known as plasma PAF acetyl hydroxylase, is a serine-dependent
 CC phospholipase which catalyses the hydrolysis of phospholipids with short
 CC chain acyl groups at the sn-2 position. Its in vivo role is not known -
 CC due to its ability to hydrolyse both phospholipids with short chain sn-2
 CC substituents (which often arise from oxidative cleavage of longer chain
 CC sn-2 substituents) and PAF. It may be either a pro-inflammatory enzyme or
 CC an anti-inflammatory enzyme, depending on the precise in vivo role
 CC adopted. LDL-PLA2 can be used in structural and mechanistic studies to
 CC elucidate the activity of the enzyme in vivo. The enzyme may be used to
 CC screen and identify compounds which modulate its activity, and to raise
 CC antibodies for use in diagnostics

XX Sequence 1361 BP; 417 A; 273 C; 278 G; 393 T; 0 U; 0 Other;

Query Match 100.0%; Score 1361; DB 3; Length 1361;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1361; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGAGAGACTAAGCTGAAGTCTGCTCAGCTCCCAAGATGGTGCACCCAAATTCGATGT 60
 Db 1 TGAGAGACTAAGCTGAAGTCTGCTCAGCTCCCAAGATGGTGCACCCAAATTCGATGT 60
 Qy 61 GCTTTTCGCTCTGGGCTGCTGGTGTGTTTATCCTTTTGACTGGCAATACATAAA 120
 Db 61 GCTTTTCGCTCTGGGCTGCTGGTGTGTTTATCCTTTTGACTGGCAATACATAAA 120
 Qy 121 TCCTGTGCCCATATGAATCATCAGCATGGTCAACAAATACAAAGTACTGATGGCTGC 180
 Db 121 TCCTGTGCCCATATGAATCATCAGCATGGTCAACAAATACAAAGTACTGATGGCTGC 180
 Qy 181 TGCAAGCTTTGGCCAAACTAAATCCCGGGGAAATGGGCTTATCCGTTGGTTGTAC 240
 Db 181 TGCAAGCTTTGGCCAAACTAAATCCCGGGGAAATGGGCTTATCCGTTGGTTGTAC 240
 Qy 241 AGACTTAATGTTGTATGATCACTAATAAGGGCACTTCTTGCGTTTATATTCATCCCA 300
 Db 241 AGACTTAATGTTGTATGATCACTAATAAGGGCACTTCTTGCGTTTATATTCATCCCA 300
 Qy 301 AGATAATGATCGCTTGACACCTTTGGATCCCAATTAAGAAATATTTTGGGGTCTTAG 360
 Db 301 AGATAATGATCGCTTGACACCTTTGGATCCCAATTAAGAAATATTTTGGGGTCTTAG 360
 Qy 361 CAAATTTCTTGGAAACACACTGGCTTATGGGCAACATTTTGAGGTTACTCTTTGGTTCAAT 420
 Db 361 CAAATTTCTTGGAAACACACTGGCTTATGGGCAACATTTTGAGGTTACTCTTTGGTTCAAT 420
 Qy 421 GACAACTCTGCAAACTGGAATTCCTCTGAGGCTGGTGAATAATTCACATTTGTTGT 480
 Db 421 GACAACTCTGCAAACTGGAATTCCTCTGAGGCTGGTGAATAATTCACATTTGTTGT 480
 Qy 481 TTTTCTCATGCTCTTGGGGCAATTCAGGACACTTTTATTCGCTATTTGGCATTTGACCTGGC 540
 Db 481 TTTTCTCATGCTCTTGGGGCAATTCAGGACACTTTTATTCGCTATTTGGCATTTGACCTGGC 540

Qy 541 ATCTCATGGGTTTATAGTTGCTGTGTAGAACACAGAGATAGATCTGCACTTGA 600
 Db 541 ATCTCATGGGTTTATAGTTGCTGTGTAGAACACAGAGATAGATCTGCACTTGA 600
 Qy 601 CTATTTCAAGGACCAATCTGCTGCAGAAATAGGGGACAAAGTCTTGCTCTACCTTAGAAC 660
 Db 601 CTATTTCAAGGACCAATCTGCTGCAGAAATAGGGGACAAAGTCTTGCTCTACCTTAGAAC 660
 Qy 661 CCTGAAACAAGAGGAGGAGACACATATACGAAATGAGCAGGTACCGCAAGCAAAAGA 720
 Db 661 CCTGAAACAAGAGGAGGAGACACATATACGAAATGAGCAGGTACCGCAAGCAAAAGA 720
 Qy 721 ATGTTCCCAAGCTCTCAGTCTGATCTTGACATGATCATGGAAGCCAGTGAAGATGC 780
 Db 721 ATGTTCCCAAGCTCTCAGTCTGATCTTGACATGATCATGGAAGCCAGTGAAGATGC 780
 Qy 781 ATTAGATTTAAAGTTTGATATGGAACAACTCAAGGACTCTATTGATAGGAAAAAATAGC 840
 Db 781 ATTAGATTTAAAGTTTGATATGGAACAACTCAAGGACTCTATTGATAGGAAAAAATAGC 840
 Qy 841 AGTAATTGGACATTTCTTTTGGTGGAGCAACGGTTATTTCAGACTCTTTAGTGAAGATCAGAG 900
 Db 841 AGTAATTGGACATTTCTTTTGGTGGAGCAACGGTTATTTCAGACTCTTTAGTGAAGATCAGAG 900
 Qy 901 ATTCAAGATGGTATTTGCCCTGGATGATGATGTTTCCACTGGGTGATGAATATATTC 960
 Db 901 ATTCAAGATGGTATTTGCCCTGGATGATGATGTTTCCACTGGGTGATGAATATATTC 960
 Qy 961 CAGAAATCTCAGGCCCTCTTTTATCAACTCTGAAATATTTCCAATATCTTGCTTAATAT 1020
 Db 961 CAGAAATCTCAGGCCCTCTTTTATCAACTCTGAAATATTTCCAATATCTTGCTTAATAT 1020
 Qy 1021 CATAAAAATGAAAAATGCTACTCACTGATATAAGAAAAAGAGATGATTACAATCAGGGG 1080
 Db 1021 CATAAAAATGAAAAATGCTACTCACTGATATAAGAAAAAGAGATGATTACAATCAGGGG 1080
 Qy 1081 TTCAGTCCACAGAAATTTTGTGCTGACTTCACTTTTGCACCTGGCAAAATATTTGGACAT 1140
 Db 1081 TTCAGTCCACAGAAATTTTGTGCTGACTTCACTTTTGCACCTGGCAAAATATTTGGACAT 1140
 Qy 1141 GCTCAAAATTAAGGGAGACATAGATTCAATATGACGCTTATTGATCTTAGCAACAAAGCTTC 1200
 Db 1141 GCTCAAAATTAAGGGAGACATAGATTCAATATGACGCTTATTGATCTTAGCAACAAAGCTTC 1200
 Qy 1201 ATTAGCATTTTACAAAAGCATTTTAGGACTTTCATAAAGATTTTGATCAGTGGGACTGCTT 1260
 Db 1201 ATTAGCATTTTACAAAAGCATTTTAGGACTTTCATAAAGATTTTGATCAGTGGGACTGCTT 1260
 Qy 1261 GATTGAAGGAGATGATGAGAAATCTTATTTCCAGGGACCAACATTAACACACCAATCAACA 1320
 Db 1261 GATTGAAGGAGATGATGAGAAATCTTATTTCCAGGGACCAACATTAACACACCAATCAACA 1320
 Qy 1321 CATCATGTTACAGAACTCTTCAGGAAATAGAGAAATACAAAT 1361
 Db 1321 CATCATGTTACAGAACTCTTCAGGAAATAGAGAAATACAAAT 1361

RESULT 3
 ABL67659

ID ABL67659 standard; DNA; 1561 BP.

XX ABL67659;

XX 15-MAY-2002 (first entry)

DE Oesophagus cancer related gene sequence SEQ ID NO:5996.

XX Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
 KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
 KW cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
 XX gene; ds.

Db 1020 AGTAATGGACATCTTTTGGTGGAGCAACGGTTATTACAGACTCTTAGTGAAGATCAGAG 1079
QY 901 ATTACAGATGGTATTCCTCGATGCATGGATGGTATTCACATGGGTGATGAATATATTC 960
Db 1080 ATTACAGATGGTATTCCTCGATGCATGGATGGTATTCACATGGGTGATGAATATATTC 1139
QY 961 CAGAATCTTCAGCCCTCTTTTATCACTCTGAATATTTCCAAATATCTCTGAATAT 1020
Db 1140 CAGAATCTTCAGCCCTCTTTTATCACTCTGAATATTTCCAAATATCTCTGAATAT 1199
QY 1021 CATAAAAATGAAAAATGCTACTCAGCTGATGAAGAAAGAAAGATCAATCAATCAGGG 1080
Db 1200 CATAAAAATGAAAAATGCTACTCAGCTGATGAAGAAAGAAAGATCAATCAATCAGGG 1259
QY 1081 TTCAGTCCACCAAGATTTTGTGACTTCACTTTTGCACCTGGCAAAATTAATTGGACAT 1140
Db 1260 TTCAGTCCACCAAGATTTTGTGACTTCACTTTTGCACCTGGCAAAATTAATTGGACAT 1319
QY 1141 GCTCAAAATTAAGGGAGACATAGATTCAAATGAGCTATGATCTTAGCAACAACTTC 1200
Db 1320 GCTCAAAATTAAGGGAGACATAGATTCAAATGAGCTATGATCTTAGCAACAACTTC 1379
QY 1201 ATTAGCATCTTACAAAAGCATTTAGGACTTCAATGAAGATTTTGTGAGTGGGACTGCTT 1260
Db 1380 ATTAGCATCTTACAAAAGCATTTAGGACTTCAATGAAGATTTTGTGAGTGGGACTGCTT 1439
QY 1261 GATTGAAGGAGATGATGAGAACTTTATTCAGGGACCAACATTAACACCAATCAACA 1320
Db 1440 GATTGAAGGAGATGATGAGAACTTTATTCAGGGACCAACATTAACACCAATCAACA 1499
QY 1321 CATCATGTTACAGAACTCTTCAGGAATAGAGAAATACAATT 1361
Db 1500 CATCATGTTACAGAACTCTTCAGGAATAGAGAAATACAATT 1540

RESULT 4

ABK92177
ID ABK92177 standard; DNA; 1505 BP.

AC ABK92177;

DT 15-AUG-2002 (first entry)

DE Prostate cancer-associated DNA sequence #63.

DE Prostate cancer; prostate tumour tissue; human; mammal; cytostatic;
KW gene therapy; gene; ds.

OS Mammalia.

XX WO200230268-A2.

PN 18-APR-2002.

XX 12-OCT-2001; 2001WO-US032045.

XX 13-OCT-2000; 2000US-00687576.

PR 08-DEC-2000; 2000US-00733288.

PR 08-DEC-2000; 2000US-00733742.

PR 24-JAN-2001; 2001US-0263957P.

PR 16-MAR-2001; 2001US-0276991P.

PR 06-APR-2001; 2001US-0281922P.

PR 24-APR-2001; 2001US-0286214P.

PR 30-APR-2001; 2001US-00847046.

PR 04-MAY-2001; 2001US-0288589P.

XX (EOSB-) EOS BIOTECHNOLOGY INC.

XX Gish KC, Mack DH, Wilson KE, Afar D, Hevezi P;

XX WPI; 2002-471335/50.

DR P-PSDB; ABG61862.

XX

PT Detecting a prostate cancer-associated transcript in a cell in a patient,
PT useful for diagnosing prostate cancer (PC) or screening modulators of PC,
PT by determining if prostate cancer-associated genes are expressed in a
PT prostate tissue.

XX Claim 22; Page 347; 436pp; English.

XX The present invention relates to methods of detecting a prostate cancer-
CC associated transcript in a cell from a patient. The method comprises
CC contacting a biological sample from the patient with prostate cancer-
CC associated polynucleotides (designated PC genes) that selectively
CC hybridize to a sequence that is at least 80% identical to them. The
CC prostate cancer-associated polynucleotide sequences are differentially
CC expressed in prostate tumour tissue or in prostate cancer and are derived
CC from the tissues of various organisms such as humans or other mammals
CC (e.g. mice, sheep and dogs). The methods of the invention are useful for
CC diagnosing and treating prostate cancer in mammals. The prostate cancer-
CC associated genes are useful for diagnosing or treating prostate cancer,
CC as well as for identifying modulators of prostate cancer or agents that
CC inhibit prostate cancer. The nucleic acid sequences are particularly
CC useful in gene therapy, as a vaccine or in antisense applications.
CC ABK92115-ABK92263 represent prostate cancer-associated polynucleotide
CC sequences

XX SQ Sequence 1505 BP; 438 A; 311 C; 333 G; 423 T; 0 U; 0 Other;

Query Match 99.9%; Score 1359.4; DB 6; Length 1505;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1360; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGAGAGACTAAGCTGAACTGCTGCTCAGCTCCAGATGGTGCCACCCAAATTCATGT 60

Db 125 TGAGAGACTAAGCTGAACTGCTGCTCAGCTCCAGATGGTGCCACCCAAATTCATGT 184

QY 61 GCTTTTCTGCTCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120

Db 185 GCTTTTCTGCTCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 244

QY 121 TCCTGTTGCCCATATGAATCATCAGCATGGGTCAACAAATACAAAGTACTGATGCTGC 180

Db 245 TCCTGTTGCCCATATGAATCATCAGCATGGGTCAACAAATACAAAGTACTGATGCTGC 304

QY 181 TGCAAGCTTTGGCCAAACTTAAATCCCGGGGAAATGGCCCTTATTCGGTTGGTTAC 240

Db 305 TGCAAGCTTTGGCCAAACTTAAATCCCGGGGAAATGGCCCTTATTCGGTTGGTTAC 364

QY 241 AGACTTAATGTTTGTATCACAATAAGGGGCACTTCTTGGCGTTTATATATATCATCCCA 300

Db 365 AGACTTAATGTTTGTATCACAATAAGGGGCACTTCTTGGCGTTTATATATATCATCCCA 424

QY 301 AGATAATGATCGCTTTGACACCCCTTTGGATCCCAATAAAGAAATATTTTGGGGTCTTAG 360

Db 425 AGATAATGATCGCTTTGACACCCCTTTGGATCCCAATAAAGAAATATTTTGGGGTCTTAG 484

QY 361 CAAATTTCTTGGAAACACATGCTTATGGGCAACATTTTGAAGTTACTCTTTGGTTCAAT 420

Db 485 CAAATTTCTTGGAAACACATGCTTATGGGCAACATTTTGAAGTTACTCTTTGGTTCAAT 544

QY 421 GACAACTCTGCNAATGGAATCCCTCTGAGGCTGGTGAATAATATCCACTTGTGT 480

Db 545 GACAACTCTGCNAATGGAATCCCTCTGAGGCTGGTGAATAATATCCACTTGTGT 604

QY 481 TTTTCTCATGGTCTTGGGGCACTTCAAGGACATTTATCTGCTATTTGGCATTCACCTGGC 540

Db 605 TTTTCTCATGGTCTTGGGGCACTTCAAGGACATTTATCTGCTATTTGGCATTCACCTGGC 664

QY 541 ATCTCATGGGTTTATAGTTGCTGCTAGAACACAGAGATAGATCTGCATCTGCAACTTA 600

Db 665 ATCTCATGGGTTTATAGTTGCTGCTAGAACACAGAGATAGATCTGCATCTGCAACTTA 724

QY 601 CTATTTCAAGGACCAATCTGCTGCAGAAATAGGGGCAAGTCTTGGCTCTACCTTAGAAC 660

Db 425 AGATAATGATCGCTTGACACCTTTGGATCCCAATAAAGAAATATTTTGGGGCTTAG 484
Qy 361 CAAATTTCTTGGAAACACACTGGCTTATGCGGCAACATTTTGGAGTTACTCTTTGGTTCAAT 420
Db 485 CAAATTTCTTGGAAACACACTGGCTTATGCGGCAACATTTTGGAGTTACTCTTTGGTTCAAT 544
Qy 421 GACAACTCTGAAACTGGAATTCCTCTGAGGCTGGTGAATAATATCCACTTTGTTGT 480
Db 545 GACAACTCTGAAACTGGAATTCCTCTGAGGCTGGTGAATAATATCCACTTTGTTGT 604
Qy 481 TTTTCTCATGCTCTTTGGGGCAATCAGGACACTTTTATCTGCTATTGGCATTGACCTGCG 540
Db 605 TTTTCTCATGCTCTTTGGGGCAATCAGGACACTTTTATCTGCTATTGGCATTGACCTGCG 664
Qy 541 ATCTCATGGTTTATAGTTGCTGTGTAGAACACAGAGATAGATCTGCATCTGCAACTTA 600
Db 665 ATCTCATGGTTTATAGTTGCTGTGTAGAACACAGAGATAGATCTGCATCTGCAACTTA 724
Qy 601 CTATTTCAAGGACCAATCTGCTGCGAATAATAGGGGCAAGCTTTGGCTCTACCTTAGAAC 660
Db 725 CTATTTCAAGGACCAATCTGCTGCGAATAATAGGGGCAAGCTTTGGCTCTACCTTAGAAC 784
Qy 661 CCTGAAACAAAGAGGAGGACACATATACGAATGAGCAGGTACGCGCAAGAGCAAAAGA 720
Db 785 CCTGAAACAAAGAGGAGGACACATATACGAATGAGCAGGTACGCGCAAGAGCAAAAGA 844
Qy 721 ATGTTCCCAAGCTCTCAGTCTGATTTGACATTTGATCATGGAAGCCAGTGAAGATGC 780
Db 845 ATGTTCCCAAGCTCTCAGTCTGATTTGACATTTGATCATGGAAGCCAGTGAAGATGC 904
Qy 781 ATTAGATTTAAAGTTTGATATGGAACAACTGAAGCACTTATGATAGGAAAAAATAGC 840
Db 905 ATTAGATTTAAAGTTTGATATGGAACAACTGAAGCACTTATGATAGGAAAAAATAGC 964
Qy 841 AGTAATTTGACACTCTTTTGGTGGAGCAACGCTTATTCAGACTCTTAGTGAAGATCAGAG 900
Db 965 AGTAATTTGACACTCTTTTGGTGGAGCAACGCTTATTCAGACTCTTAGTGAAGATCAGAG 1024
Qy 901 ATTCAGATGTGGTATTTGCCCTGGATGCGATGTTTCCACTGGGTGATGAAGTATATTC 960
Db 1025 ATTCAGATGTGGTATTTGCCCTGGATGCGATGTTTCCACTGGGTGATGAAGTATATTC 1084
Qy 961 CAGAAATTCCTCAGCCCTCTTTTATCAACTCTGAATTTCCAAATATTCCTGCTAAAT 1020
Db 1085 CAGAAATTCCTCAGCCCTCTTTTATCAACTCTGAATTTCCAAATATTCCTGCTAAAT 1144
Qy 1021 CATAAAAATGAAAAATGCTACTCCTGATGAAGAAAGAAAGATGATTACAAATCAGGG 1080
Db 1145 CATAAAAATGAAAAATGCTACTCCTGATGAAGAAAGAAAGATGATTACAAATCAGGG 1204
Qy 1081 TTCAGTCCCAAGAAATTTTGGCTGACTTCACTTTTGCACCTGGCAAAATAATTTGGACAT 1140
Db 1205 TTCAGTCCCAAGAAATTTTGGCTGACTTCACTTTTGCACCTGGCAAAATAATTTGGACAT 1264
Qy 1141 GCTCAAAATTAAGGAGACATAGATTCAATCAGCTATTGATCTTAGCAACAAGGCTTC 1200
Db 1265 GCTCAAAATTAAGGAGACATAGATTCAATCAGCTATTGATCTTAGCAACAAGGCTTC 1324
Qy 1201 ATTAGCATTCTTACAAAGCAATTTAGGACTTCAATAAGATTTTGTATCAGTGGGACTGTT 1260
Db 1325 ATTAGCATTCTTACAAAGCAATTTAGGACTTCAATAAGATTTTGTATCAGTGGGACTGTT 1384
Qy 1261 GATTGAAGGAGATGATGAGAACTTTATTCAGGGACCAACATTAACACCAACCAATCAACA 1320
Db 1385 GATTGAAGGAGATGATGAGAACTTTATTCAGGGACCAACATTAACACCAACCAATCAACA 1444
Qy 1321 CATCATGTTACAGAACTCTTTCAGGAATAGAGAAATACAAAT 1361
Db 1445 CATCATGTTACAGAACTCTTTCAGGAATAGAGAAATACAAAT 1485

ADP65357
ID ADP65357 standard; DNA; 1505 BP.
XX AC ADP65357;
XX DT 12-AUG-2004 (first entry)
XX DE Human platelet-activating factor acetylhydrolase mRNA, complete DNA.
XX KW autoimmune disease; arthritis; gene expression analysis;
XX KW rheumatoid arthritis; collagen-induced; immunosuppressive; antirheumatic;
XX KW antiarthritic; osteopathic; antitumor; antiinflammatory; dermatological;
XX KW immunomodulatory; lupus; ankylosing spondylitis; fibrositis;
XX KW fibromyalgia; osteoarthritis; gout; juvenile rheumatoid arthritis;
XX KW immune; ds; human.
XX OS Homo sapiens.
XX PN WO2003072827-A1.
XX PD 04-SEP-2003.
XX PF 31-OCT-2002; 2002WO-US035433.
XX PR 31-OCT-2001; 2001US-0336220P.
XX PA (CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.
XX PI Hirsch R, Thorton SL;
XX DR WPI; 2003-712740/67.
XX DR GENBANK; U20157.
XX PT Diagnosing and analyzing autoimmune disease using gene expression
XX PT profiles and microarray technology, useful for diagnosing and treating
XX PT rheumatoid arthritis, lupus, fibrositis, osteoarthritis, fibromyalgia and
XX PT gout.
XX PS Disclosure; Page; 56pp; English.
XX CC The invention relates to a novel method for diagnosing and analysing
XX CC autoimmune disease or arthritides. The method comprises obtaining a
XX CC patient sample containing mRNA, analysing gene expression using the mRNA
XX CC that results in a gene expression signature of the mRNA, and using that
XX CC gene expression signature to diagnose or analyse the autoimmune disease
XX CC or arthritides in the patient, where gene expression of at least 60% of
XX CC the genes correlates with that of the gene signature. The invention
XX CC further comprises: a treatment of rheumatoid arthritis; identification of
XX CC genes for targeting in the treatment of rheumatoid arthritis in a mammal
XX CC other than a mouse; diagnosis of rheumatoid arthritis in a mammal; an
XX CC array or gene chip, specific for rheumatoid arthritis; diagnosis or
XX CC analyses of autoimmune disease or rheumatoid arthritis; screening the
XX CC efficacy of a candidate drug in vitro for the treatment of collagen-
XX CC induced arthritis; and reducing the symptoms associated with collagen-
XX CC induced arthritis. The compositions of the invention have the following
XX CC activities: immunosuppressive, antirheumatic, antitumor, osteopathic,
XX CC antitumor, antiinflammatory, dermatological, and immunomodulatory. The
XX CC methods and compositions of the present invention are useful for
XX CC diagnosing and treating autoimmune disease or arthritides, such as
XX CC rheumatoid arthritis, lupus, ankylosing spondylitis, fibrositis,
XX CC fibromyalgia, osteoarthritis, gout, juvenile rheumatoid arthritis, and an
XX CC immune disease caused by an infectious agent. This polynucleotide
XX CC represents a DNA sequence relating to the genes used in the analysis and
XX CC treatment of autoimmune diseases or arthritides. Note: This sequence is
XX CC not shown in the specification. It has been supplied in an electronic
XX CC format from WIPO.

SQ Sequence 1505 BP; 438 A; 311 C; 333 G; 423 T; 0 U; 0 Other;
Query Match 99.9%; Score 1359.4; DB 11; Length 1505;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1360; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

(BRIM) BRISTOL-MYERS SQUIBB CO.
 Nadler SG, Neubauer MG, Feder JN, Carman J;
 WPI; 2004-562168/54.
 P-PSDB; ADRI4277.
 New isolated polynucleotides and polypeptides associated with NF-kappaB pathway, useful for diagnosing, treating, or preventing disorders or diseases associated with NF-kappaB pathway.
 Claim 1; SEQ ID NO 277; 237bp; English.
 This invention relates to the novel association of protein sequences (and the genes which encode them) to the NF-kappaB pathway. The invention may be useful for the production of compounds with an antiinflammatory, cytostatic, hepatotropic, virucide, antiarthritic, antirheumatic, gastrointestinal-Gen, antiaesthetic, antiarteriosclerotic, immunomodulator, cerebroprotective, vasotropic, immunosuppressive or vulnary activity or for gene therapy. The proteins and nucleotides are useful for diagnosing, preventing, treating, or ameliorating conditions or diseases associated with the NF-kappaB pathway. The condition is an immune disorder, an inflammatory disorder, an inflammatory disorder related to aberrant NF-kappaB regulation, cancer, aberrant apoptosis, hepatic disorders, Hodgkin's lymphomas, haematopoietic tumours, hyper-IgM syndromes, hypohidrotic ectodermal dysplasia, X-linked anhidrotic ectodermal dysplasia, immunodeficiency, viral infections, HIV-1, HTLV-1, hepatitis B, hepatitis C, EBV, influenza, viral replication, host cell survival, evasion of immune responses, rheumatoid arthritis, inflammatory bowel disease, colitis, asthma, atherosclerosis, cachexia, euthyroid sick syndrome, stroke, EAE, autoimmune disorders, disorders related to hyper immune activity, disorders related to aberrant acute phase responses, hypercongenital conditions, birth defects, necrotic lesions, wounds, organ transplant rejection, conditions related to organ transplant rejection, disorders related to aberrant signal transduction, proliferating disorders, cancers and HIV propagation in cells infected with other viruses. The present sequence is that of a human gene which is subject to the novel association with the NF-kappaB pathway of the invention. Note: This sequence does not appear in the specification but was obtained by the indexer from Genbank.

Query Match 99.9%; Score 1359.4; DB 13; Length 1505;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1360; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 TGAGAGACTAAGCTGAACTGCTCAGCTCCAGATGGTGCACCCCAATTCATCT 60
 125 TGAGAGACTAAGCTGAACTGCTCAGCTCCAGATGGTGCACCCCAATTCATCT 184
 61 GCTTTTCTGCTCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
 185 GCTTTTCTGCTCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 244
 121 TCCTGTTGCCATATCAAAATCATCAGATGGTGCACCAAAATCAAGTACTGATGCTGC 180
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 181 TCGAAGCTTTGGCCAACTAAATATCCCGGGGAATGGCCCTTATTCGTTGGTTGTAC 240
 305 TCGAAGCTTTGGCCAACTAAATATCCCGGGGAATGGCCCTTATTCGTTGGTTGTAC 364
 241 AGACTTAATGTTTGATCACAATAAGGCACCTTTCTTGGCTTATATATATCCATCCCA 300
 365 AGACTTAATGTTTGATCACAATAAGGCACCTTTCTTGGCTTATATATATCCATCCCA 424
 301 AGATAATGATCGCTTTGACACCTTTTGGATCCCAATAAAGATATTTTTGGGGCTTAG 360
 425 AGATAATGATCGCTTTGACACCTTTTGGATCCCAATAAAGATATTTTTGGGGCTTAG 484
 361 CAAATTTCTTGGAAACACACTGGCTTATGGCAACATTTTGAGGTTACTCTTTGGTTCAAT 420

485 CAAATTTCTTGGAAACACACTGGCTTATGGCAACATTTTGAGGTTACTCTTTGGTTCAAT 544
 421 GACAACTCTCGCAAACTGGAATTCCTCTGAGGCTGCTGGAATAATATCCACTTTGTT 480
 545 GACAACTCTCGCAAACTGGAATTCCTCTGAGGCTGCTGGAATAATATCCACTTTGTT 604
 481 TTTTCTCATGCTCTTGGGCACTCAGGACATTTTATCTGCTTATTTGCAATTTGACCTGGC 540
 605 TTTTCTCATGCTCTTGGGCACTCAGGACATTTTATCTGCTTATTTGGCAATTTGACCTGGC 664
 541 ATCTCATGCTTTATAGTTGCTGCTGAGAAACACAGAGATAGATCTGCACTCTGCAACTTA 600
 665 ATCTCATGCTTTATAGTTGCTGCTGAGAAACACAGAGATAGATCTGCACTCTGCAACTTA 724
 601 CTATTTCAAGGACCAATCTGCTGAGAAATAGGGGCAAGTCTTGGCTCTTACCTTAGAAC 660
 725 CTATTTCAAGGACCAATCTGCTGAGAAATAGGGGCAAGTCTTGGCTCTTACCTTAGAAC 784
 661 CCTGAAACCAAGAGGAGGAGACATATAGCAATGAGAGGCTACCGCAAGAGCAAAAGA 720
 785 CCTGAAACCAAGAGGAGGAGACATATAGCAATGAGAGGCTACCGCAAGAGCAAAAGA 844
 721 ATGTTTCCCAAGCTCTCAGTCTCATTTTGCATTTGATCATGAAAGCCAGTGAAGATGC 780
 845 ATGTTTCCCAAGCTCTCAGTCTCATTTTGCATTTGATCATGAAAGCCAGTGAAGATGC 904
 781 ATTAGATTTAAAGTTTGAATATGGAACCACTGAAGGACTCTATTGATAGGAAAAATAGC 840
 905 ATTAGATTTAAAGTTTGAATATGGAACCACTGAAGGACTCTATTGATAGGAAAAATAGC 964
 841 AGTAATTTGACATCTCTTTGGTGGAGCAACGGTTATTCAGACTCTTAGTGAAGATCAGAG 900
 965 AGTAATTTGACATCTCTTTGGTGGAGCAACGGTTATTCAGACTCTTAGTGAAGATCAGAG 1024
 901 ATTGAGATCTGCTATTGCTGCTGATGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
 1025 ATTGAGATCTGCTATTGCTGCTGATGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCT 1084
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 1085 CAGAAATTCCTCAGCCCTCTTTTTTATCAACTCTGAATATTTTCCAAATATCTGCTTAAT 1144
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 1205 TTCAGTCCACCAAGATTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1264
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 1265 GCTCAAAATTAAGGGGAGACATAGATTTCAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1324
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 1325 ATTAGATCTTTAAGAAAGCTTTAGGACTCTTAAGATTTTGTGCTGCTGCTGCTGCTGCTGCT 1384
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 1385 GATTGAAGGAGATGATGAGAACTTTATTCAGGGACCAACATTTAACAACCAATCAACA 1444
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RESULT 12
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 ID ADP54610 standard; cdna; 1505 bp.
 XX
 AC ADP54610;
 XX

Qy	1141	GCTCAAAATTAAAGGGAGACATAGATTCAAATGACGCTATTGATCTTAGCAACAAGCTTC	1200
Db	1265	GCTCAAAATTAAAGGGAGACATAGATTCAAATGTGATCTTAGCAACAAGCTTC	1324
Qy	1201	ATTAGCAATCTTACAAAGAAGCATTTAGGACCTTCATAAAGATTTTGATCAGTGGGACTGCTT	1260
Db	1325	ATTAGCAATCTTACAAAGAAGCATTTAGGACCTTCATAAAGATTTTGATCAGTGGGACTGCTT	1384
Qy	1261	GATTGAAGGAGATGATGAGAATCTTATTTCAGGGACCAACATTAAACAACAACCAATCAACA	1320
Db	1385	GATTGAAGGAGATGATGAGAATCTTATTTCAGGGACCAACATTAAACAACAACCAATCAACA	1444
Qy	1321	CATCATGTTTACAGAACTCTTCAGGAATAGAGAATACAATTT	1361
Db	1445	CATCATGTTTACAGAACTCTTCAGGAATAGAGAATACAATTT	1485

RESULT 13

ADP23966
ID ADP23966 standard; cDNA; 1505 BP.

AC ADP23966:

DT 18-NOV-2004 (first entry)

DE PRO polypeptide encoding cDNA SEQ ID NO:1144.

ss; gene; PRO; antiinflammatory; antiarthritic; antirheumatic;
KW immunosuppressive; osteopathic; antidiabetic; dermatological;
KW antipsoriatic; antiallergic; antiasthmatic; hepatotropic; respiratory;
KW gene therapy; immune system.

OS Unidentified.

XX PN WO2004041170-A2.

21-MAY-2004.

30-OCT-2003: 2003WO-US034312.

01-NOV-2002: 2002US-0423394P.

PA (GETH) GENENTECH INC.

PI Clark H, Schoenfeld J, Van Lookeren M, Williams PM, Wood WI;
PI Wu TD;

DR WPI; 2004-419628/39.

XX
F-FORD, ADF23307.

PT New PRO polypeptides and polynucleotides, useful for treating e.g.
PT erythematous, rheumatoid arthritis, diabetes mellitus, immune-mediated
PT renal disease, or demyelinating diseases of the central or peripheral
PT nervous system.

PS Claim 1; SEQ ID NO 1144; 2940pp; English.

The invention relates to a novel isolated nucleic acid and the PRO polypeptide encoded by it. A protein of the invention has antiinflammatory, antiarthritic, antirheumatic, immunosuppressive, osteopathic, antiadipatic, dermatological, antispasmodic, antiallergic, antiasthmatic, hepatotropic, and respiratory activity. A polynucleotide of the invention may have a use in gene therapy. The PRO polypeptide, its agonist, antagonist, or antibody that specifically binds to the polypeptide is useful for treating an immune related disorder such as systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an idiopathic inflammatory myopathy, Sjogren's syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, a demyelinating disease of the central or peripheral nervous system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome, CC

Db 905 ATTAGATTAAAGTTTGATATGGAACAACAGGACTCTATTGATAGGGAATAATAGC 964
 QY 841 AGTAATTTGACATCTCTTTTGGTGGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAG 900
 Db 965 AGTAATTTGACATCTCTTTTGGTGGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAG 1024
 QY 901 ATTGAGATGTGATTGCCCCCTGGATGTCATGGAATGTTTCCACTGGGTGATGAAGTATATTC 960
 Db 1025 ATTGAGATGTGATTGCCCCCTGGATGTCATGGAATGTTTCCACTGGGTGATGAAGTATATTC 1084
 QY 961 CAGNATTTCTCAGCCCTCTTTTATCACTCTGAATATTTCCATATCTCTGCTAATAT 1020
 Db 1085 CAGAATTTCTCAGCCCTCTTTTATCACTCTGAATATTTCCATATCTCTGCTAATAT 1144
 QY 1021 CATAAAAATGAATAATGCTACTCACCTGATAAAGAAAGAAAGATGATTACAATCAGGGG 1080
 Db 1145 CATAAAAATGAATAATGCTACTCACCTGATAAAGAAAGAAAGATGATTACAATCAGGGG 1204
 QY 1081 TTGAGTCCACCAAGATTTTGTGACTTCACTTTTGGCACTGGCAAAATATTTGGACACAT 1140
 Db 1205 TTGAGTCCACCAAGATTTTGTGACTTCACTTTTGGCACTGGCAAAATATTTGGACACAT 1264
 QY 1141 GCTCAAAATTAAGGGAGACATAGATTCRAATGACGCTATTGATCTTAGCAACAAGACTTC 1200
 Db 1265 GCTCAAAATTAAGGGAGACATAGATTCRAATGACGCTATTGATCTTAGCAACAAGACTTC 1324
 QY 1201 ATTAGCATTTCTACAAAAGCATTTAGGACTTCTAAGAGATTTTGATCAGTGGGACTGCTT 1260
 Db 1325 ATTAGCATTTCTACAAAAGCATTTAGGACTTCTAAGAGATTTTGATCAGTGGGACTGCTT 1384
 QY 1261 GATTGAAGGAGATGATGAATCTTTATTCAGGGACCAACATTAACACCAACCAATCAACA 1320
 Db 1385 GATTGAAGGAGATGATGAATCTTTATTCAGGGACCAACATTAACACCAACCAATCAACA 1444
 QY 1321 CATCATGTTACAGAACTCTTCAGGAATAGAGAAATACAATT 1361
 Db 1445 CATCATGTTACAGAACTCTTCAGGAATAGAGAAATACAATT 1485

RESULT 14

ID AAQ87947 standard; cdna; 1520 BP.
 AC AAQ87947;

XX 25-MAR-2003 (revised)
 DT 06-DEC-1995 (first entry)

XX Human platelet activating factor, acetyl hydrolase (PAF-AH), cDNA.

XX Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;
 KW disease; pleurisy; diagnosis, ss.
 XX Homo sapiens.

FH Key Location/Qualifiers

FT CDS 162..1487

FT /*tag= a

FT /product= "Acetyl_hydrolase."

XX W09509921-A1.

XX 13-APR-1995.

XX 06-OCT-1994; 94WO-US011340.

XX 06-OCT-1993; 93US-00133803.

XX (ICOS-) ICOS CORP.

XX Cougens LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;

XX Wilder CL;

DR WPI; 1995-155262/20.
 DR P-PSDB; AAR71913.
 XX New nucleic acid encoding platelet activating factor, acetyl hydrolase -
 PT useful in diagnosis and for treating inflammatory diseases, e.g.
 PT pleurisy.
 XX Claim 4; Page 51-53; 88pp; English.
 CC The human acetyl hydrolase gene (AAQ87947) has been isolated and
 CC purified. The platelet activating factor acetyl hydrolase (AAR71913) is
 CC useful in the treatment of inflammatory diseases, in particular pleurisy,
 CC asthma, rhinitis and eczema. The gene may also be used in raising
 CC monoclonal antibodies specific for PAF-AH that are useful in the
 CC diagnosis of such diseases. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 1520 BP; 453 A; 311 C; 333 G; 423 T; 0 U; 0 Other;

Query Match 99.9%; Score 1359.4; DB 2; Length 1520;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1360; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 61 GCTTTTCTGCTCTCTCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120

Db 185 GCTTTTCTGCTCTCTCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 244

QY 121 TCCTTTGCCCATATGAATCATAGCATGGGTCAACAAATATAAGTACTGATGGTGC 180

Db 245 TCCTTTGCCCATATGAATCATAGCATGGGTCAACAAATATAAGTACTGATGGTGC 304

QY 181 TGCAGCTTTGGCCAAACTTAAATCCCGGGGAAATGGGCTTATTCGTTGGTTGTAC 240

Db 305 TGCAGCTTTGGCCAAACTTAAATCCCGGGGAAATGGGCTTATTCGTTGGTTGTAC 364

QY 241 AGACTTAATGTTTGATCACACTTAATAGGGGACCTTTCTTGGCTTTATATATTCATCCCA 300

Db 365 AGACTTAATGTTTGATCACACTTAATAGGGGACCTTTCTTGGCTTTATATATTCATCCCA 424

QY 301 AGATAATGATCGCTTTGACACCTTTTGGATCCCAATAAAGAAATATTTTGGGGCTTTAG 360

Db 425 AGATAATGATCGCTTTGACACCTTTTGGATCCCAATAAAGAAATATTTTGGGGCTTTAG 484

QY 361 CAAATTTCTTGGAAACACACTGCTTTATGGGCAACATTTTGAGGTTACTCTTTTGGTTCAAT 420

Db 485 CAAATTTCTTGGAAACACACTGCTTTATGGGCAACATTTTGAGGTTACTCTTTTGGTTCAAT 544

QY 421 GACAACTCTGCAAACTGGAATTCCTCTGAGGCTGCTGAGGCTGCTGAGGCTGCTGAGGCT 480

Db 545 GACAACTCTGCAAACTGGAATTCCTCTGAGGCTGCTGAGGCTGCTGAGGCTGCTGAGGCT 604

QY 481 TTTTCTCATGGTCTTTGGGGCAATTCAGGACACTTTTATCTGCTATTTGCAATTCAGCTGCG 540

Db 605 TTTTCTCATGGTCTTTGGGGCAATTCAGGACACTTTTATCTGCTATTTGCAATTCAGCTGCG 664

QY 541 ATCTCATGGTCTTTATAGTTGCTGCTAGAACACAGAGATAGATCTGATCTGCAACTTGA 600

Db 665 ATCTCATGGTCTTTATAGTTGCTGCTAGAACACAGAGATAGATCTGATCTGCAACTTGA 724

QY 601 CTATTTTCAAGGACCAATCTGCTGCAAGAAATAGGGGACCAAGTCTTGGCTCTACCTTAGAAC 660

Db 725 CTATTTTCAAGGACCAATCTGCTGCAAGAAATAGGGGACCAAGTCTTGGCTCTACCTTAGAAC 784

QY 661 CCTGAAACAAGAGAGAGAGACACATATACGAAATGAGCAGGTACCGGCAAGAGCAAAAGA 720

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QY 721 ATGTTTCCCAAGCTCTCAGTCTGATTCTTGGACATTCATCATGAAAGCCAGTGAAGATGC 780

Db 845 ATGTTTCCCAAGCTCTCAGTCTGATTCTTGGACATTCATCATGAAAGCCAGTGAAGATGC 904


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Db      ||||| 725 CTATTTTCAAGGACCAATCTGCTCAGAAATAGGGGCAAGTCTTTGGCTCTACCTTAGAAC 784
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 Job time : 886.202 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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(without alignments)
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1361	100.0	1361	2	US-08-387-858A-9
3	1361	100.0	1361	3	US-09-294-384B-9
4	1361	100.0	1361	3	US-08-717-079-9
5	1359.4	99.9	1520	1	US-08-470-187-7
6	1359.4	99.9	1520	1	US-08-318-905-7
7	1359.4	99.9	1520	1	US-08-483-232-7
8	1359.4	99.9	1520	1	US-08-483-140-7
9	1359.4	99.9	1520	2	US-08-485-938A-7
10	1359.4	99.9	1520	2	US-08-910-041-7
11	1359.4	99.9	1520	3	US-09-328-474-7
12	1359.4	99.9	1520	3	US-09-100-546-7
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ALIGNMENTS

RESULT 1
US-08-557-892-9
; Sequence 9, Application US/08557892
; Patent No. 5968818
; GENERAL INFORMATION:
; APPLICANT: MacPhee, Colin Houston
; APPLICANT: Tew, David Graham
; APPLICANT: Southan, Christopher Donald
; APPLICANT: Hickey, Dierdre Mary Bernadette
; APPLICANT: Gloger, Israel Simon
; APPLICANT: Lawrence, Geoffrey Mark Prouse
; APPLICANT: Rice, Simon Quentyn John
; TITLE OF INVENTION: Compounds
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/557,892
; FILING DATE: 14 No. 5968818ember 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/387,858
; FILING DATE: 14 No. 5968818ember 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dustman, Wayne J.
; REGISTRATION NUMBER: 33,870
; REFERENCE/DOCKET NUMBER: P30693C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5023
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1361 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO

TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 38..1360
US-08-387-858A-9

Query Match 100.0%; Score 1361; DB 2; Length 1361;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1361; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 TGAGAGACTAAGCTGAACTGCTCAGCTCCCAAGATGGTGCACCCAAATTCATGT 60
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Db 61 GCTTTTCGCTCTCGCGGCTCGCTGGCTGTGGTTTATCTCTTTGACCTGGCAATACATAA 120
Qy 121 TCCTGTTGCCATATGAATCATCAGCATGGGTCAACAAATACAAAGTACTGATGGCTGC 180
Db 121 TCCTGTTGCCATATGAATCATCAGCATGGGTCAACAAATACAAAGTACTGATGGCTGC 180
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Db 301 AGATAATGATCGCTTGACACCCCTTTGGATCCCAATAAAGAAATATTTTGGGCTCTAG 360
Qy 361 CAAATTTCTTGGAAACACACTGGCTTATGGGCAACATTTTGGGTTACTCTTTGGTTCAAT 420
Db 361 CAAATTTCTTGGAAACACACTGGCTTATGGGCAACATTTTGGGTTACTCTTTGGTTCAAT 420
Qy 421 GACAACTCTGCAAACTGGAATCCCTCTGAGGCTGGTGAATAATATCCACTTGTGT 480
Db 421 GACAACTCTGCAAACTGGAATCCCTCTGAGGCTGGTGAATAATATCCACTTGTGT 480
Qy 481 TTTTCTCATGCTCTGGGGCATTCAGGACACTTTTATCTGCTATTGGCAATTCACCTGGC 540
Db 481 TTTTCTCATGCTCTGGGGCATTCAGGACACTTTTATCTGCTATTGGCAATTCACCTGGC 540
Qy 541 ATCTCATGGTTTATAGTTGCTGCTGTPAGAACACAGAGATAGATCTGCACTCTCAACTTA 600
Db 541 ATCTCATGGTTTATAGTTGCTGCTGTPAGAACACAGAGATAGATCTGCACTCTCAACTTA 600
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Db 601 CTATTTCAAGCAACCAATCTGTCAGAAATAGGGGCAAGCTCTTGGCTCTACCTTAGAAC 660
Qy 661 CCTGAAACAGAGAGAGAGACACATATACAAATAGCAGGTAGCGGCAAGAGACAAAGA 720
Db 661 CCTGAAACAGAGAGAGAGACACATATACAAATAGCAGGTAGCGGCAAGAGACAAAGA 720
Qy 721 ATGTTCCCAAGCTCTCAGTCTGATTTCTGATCATGTTGATGTTGATGTTGATGTTGATG 780
Db 721 ATGTTCCCAAGCTCTCAGTCTGATTTCTGATCATGTTGATGTTGATGTTGATGTTGATG 780
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Db 781 ATTAGATTTAAGTTGATATGAACTAGAGGACTCTTATGATAGGGAATAATAGC 840
Qy 841 AGTAATTGGACATTTCTTTGGTGGAGCAACGGTTATTCAGACTCTTAGTGAAGTACAG 900
Db 841 AGTAATTGGACATTTCTTTGGTGGAGCAACGGTTATTCAGACTCTTAGTGAAGTACAG 900

Db 841 AGTAATTGGACATTTCTTTGGTGGAGCAACGGTTATTCAGACTCTTAGTGAAGTACAG 900
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Db 901 ATTCAAGATGGTATTTGCCCTGGATGATGATGTTTCCACTGGTGGTGAAGTATATTC 960
Qy 961 CAGAAATTCCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAAATATCTGCTATAT 1020
Db 961 CAGAAATTCCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAAATATCTGCTATAT 1020
Qy 1021 CATAAAAATGAAAAAATGCTACTCACCTGATAAAGAAAGAAAGATGATTACAATCAGGG 1080
Db 1021 CATAAAAATGAAAAAATGCTACTCACCTGATAAAGAAAGAAAGATGATTACAATCAGGG 1080
Qy 1081 TTCAGTCCACCAAGATTTTGGCTGACTCTTCTTGGCAACTGGCAAAATTAATGGACACAT 1140
Db 1081 TTCAGTCCACCAAGATTTTGGCTGACTCTTCTTGGCAACTGGCAAAATTAATGGACACAT 1140
Qy 1141 GCTCAATTAAGGGAGACATAGATTCAAAATGAGCTATTGATCTTTAGCAACAAAGCTTC 1200
Db 1141 GCTCAATTAAGGGAGACATAGATTCAAAATGAGCTATTGATCTTTAGCAACAAAGCTTC 1200
Qy 1201 ATTAGCATTTTACAAAAGCATTTAGGACTTTTATAAAGATTTTGTAGTGGGACTGCTT 1260
Db 1201 ATTAGCATTTTACAAAAGCATTTAGGACTTTTATAAAGATTTTGTAGTGGGACTGCTT 1260
Qy 1261 GATTGAAGGAGATGATGAGAAATCTTATTCAGGGACCAACATTAAACAACCAATCAACA 1320
Db 1261 GATTGAAGGAGATGATGAGAAATCTTATTCAGGGACCAACATTAAACAACCAATCAACA 1320
Qy 1321 CATCATGTTTACAGAACTCTTCAGGAATAGAGAAATACAATT 1361
Db 1321 CATCATGTTTACAGAACTCTTCAGGAATAGAGAAATACAATT 1361

RESULT 3

US-09-294-384B-9
; Sequence 9, Application US/09294384B
; Patent No. 6177257
; GENERAL INFORMATION:
; APPLICANT: MacPhee, Colin Houston
; APPLICANT: Tew, David Graham
; APPLICANT: Southan, Christopher Donald
; APPLICANT: Hickey, Dierdre Mary Bernadette
; APPLICANT: Glozier, Israel Simon
; APPLICANT: Lawrence, Geoffrey Mark Prouse
; APPLICANT: Rice, Simon Quentyn John
; TITLE OF INVENTION: Compounds
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/294,384B
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/387,858
; FILING DATE: 24 February 1995
; APPLICATION NUMBER: PCT/GB94/01374
; FILING DATE: 24 June 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dustman, Wayne J.
; REGISTRATION NUMBER: 33,870

```

; REFERENCE/DOCKET NUMBER: P30693
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5023
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1361 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 38..1360
; US-09-294-384B-9

Query Match 100.0%; Score 1361; DB 3; Length 1361;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1361; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGAGAGACTAAGCTGAACTGCTCAGCTCCCAAGATGGTCCACCCAAATTCATGT 60
DB 1 TGAGAGACTAAGCTGAACTGCTCAGCTCCCAAGATGGTCCACCCAAATTCATGT 60

QY 61 GCTTTTCGCTCTGGGCTGCTGGCTGGTGGTTTATCCTTTTGACTGGCAATACATAA 120
DB 61 GCTTTTCGCTCTGGGCTGCTGGCTGGTGGTTTATCCTTTTGACTGGCAATACATAA 120

QY 121 TCCTGTGGCCATATGAATCATCAGCATGGGTCAACAAATACAAATACAGTACTGCTGC 180
DB 121 TCCTGTGGCCATATGAATCATCAGCATGGGTCAACAAATACAAATACAGTACTGCTGC 180

QY 181 TGCAAGCTTTGGCCAACTAAATCCCGGGGAAATGGGCCCTTATTCGGTTGGTAC 240
DB 181 TGCAAGCTTTGGCCAACTAAATCCCGGGGAAATGGGCCCTTATTCGGTTGGTAC 240

QY 241 AGACTTAATGTTTGATCACAATTAAGGCACTCTTCGGTTTATATATATCCATCCCA 300
DB 241 AGACTTAATGTTTGATCACAATTAAGGCACTCTTCGGTTTATATATATCCATCCCA 300

QY 301 AGATAATGATCGCTTGACACCTTTGGATCCCAATTAAGAAATATTTTGGGGTCTTAG 360
DB 301 AGATAATGATCGCTTGACACCTTTGGATCCCAATTAAGAAATATTTTGGGGTCTTAG 360

QY 361 CAAATTTCTTGGAAACACACTGGCTTATGGGCAACATTTTGAGGTACTCTTTGGTTCAAT 420
DB 361 CAAATTTCTTGGAAACACACTGGCTTATGGGCAACATTTTGAGGTACTCTTTGGTTCAAT 420

QY 421 GACAACTCCGCAACTGGATTCCTCTGAGGCTGGTGAANAATATCCATCTGTTGT 480
DB 421 GACAACTCCGCAACTGGATTCCTCTGAGGCTGGTGAANAATATCCATCTGTTGT 480

QY 481 TTTTTCATGGTCTTGGGCACTTCAGGACATTTTATCTGCTATTGGCAATTCACCTGGC 540
DB 481 TTTTTCATGGTCTTGGGCACTTCAGGACATTTTATCTGCTATTGGCAATTCACCTGGC 540

QY 541 ATCTCATGGTTTATAGTGTGCTGTPAGAACACAGAGATAGATCTGCAATCTGCAACTTA 600
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DB 661 CCTGAACAAGAGGAGGAGACACATATACAAATAGCAGGTACGGCAAGAGCAAAAGA 720

QY 721 ATGTTCCCAAGCTCTCAGTCTGATCTTGTGATGATCGAAGCCAGTGAAGATGC 780

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DB 721 ATGTTCCCAAGCTCTCAGTCTGATCTTGTGACATTCATGGAAGCCAGTGAAGATGC 780
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DB 781 ATTAGATTTAAAGTTTGTATATGGAACAACCTGAAGGACTCTATTGTAGGAAAAAATAGC 840
QY 841 AGTAATTTGACATTTCTTTTGGTGGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAG 900
DB 841 AGTAATTTGACATTTCTTTTGGTGGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAG 900
QY 901 ATTCAAGATGTGTATTCCTCGGATGTCAGTGGATGTTTCCACTGGGTGATGATATATTC 960
DB 901 ATTCAAGATGTGTATTCCTCGGATGTCAGTGGATGTTTCCACTGGGTGATGATATATTC 960
QY 961 CAGAAATTCCTCAGCCCTCTTTTATCAACTCTGAATATTTCCCAATATCTCTGCTAATAT 1020
DB 961 CAGAAATTCCTCAGCCCTCTTTTATCAACTCTGAATATTTCCCAATATCTCTGCTAATAT 1020
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DB 1021 CATAAAAATGAAAAATGCTACTCACCCTGATATAAGAAAAAGAGATGATTACAATCAGGGG 1080
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DB 1081 TTCAAGTCCACCAAGATTTTGTGCTGACTTCACTTTTGCACCTGGCAAAATTAATTGGACAT 1140
QY 1141 GCTCAAAATTAAGGGAGACATAGATTCAAAATCAGCTATTGATCTTAGCAACAAAGCTTC 1200
DB 1141 GCTCAAAATTAAGGGAGACATAGATTCAAAATCAGCTATTGATCTTAGCAACAAAGCTTC 1200
QY 1201 ATTAGCATTTTACAAAAGCATTTAGGACTTCATAAAGATTTTGTAGTCACTGGGACTGCTT 1260
DB 1201 ATTAGCATTTTACAAAAGCATTTAGGACTTCATAAAGATTTTGTAGTCACTGGGACTGCTT 1260
QY 1261 GATTGAAGAGATGATGAGAACTTTATTCAGGGACCAACATTAACACCAACCAATCAACA 1320
DB 1261 GATTGAAGAGATGATGAGAACTTTATTCAGGGACCAACATTAACACCAACCAATCAACA 1320
QY 1321 CATCATGTTTACAGAACTCTTCAGGAATAGAGAAATACAATT 1361
DB 1321 CATCATGTTTACAGAACTCTTCAGGAATAGAGAAATACAATT 1361

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RESULT 4

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US-08-717-079-9
; Sequence 9, Application US/08717079
; Patent No. 638045
; GENERAL INFORMATION:
; APPLICANT: MacPhee, Colin Houston
; APPLICANT: Tew, David Graham
; APPLICANT: Southan, Christopher Donald
; APPLICANT: Hickey, Dierdre Mary Bernadette
; APPLICANT: Gloger, Israel Simon
; APPLICANT: Lawrence, Geoffrey Mark Prouse
; APPLICANT: Rice, Simon Quentyn John
; TITLE OF INVENTION: Compounds
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/717,079
; FILING DATE:
; CLASSIFICATION: 435

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COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/470,187
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: No. 5532152and, Greta E.
 REGISTRATION NUMBER: 35,302
 REFERENCE/DOCKET NUMBER: 31672
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (312) 474-6300
 TELEFAX: (312) 474-0448
 TELEX: 25-3658
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1520 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 162..1484
 US-08-470-187-7

Query Match 99.9%; Score 1359.4; DB 1; Length 1520;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1360; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 TGAGAGACTAAGCTGAACTGCTCAGCTCCCAAGATGGTCCACCCAAATTCATGT 60
 125 TGAGAGACTAAGCTGAACTGCTCAGCTCCCAAGATGGTCCACCCAAATTCATGT 184
 61 GCTTTTCTGCTCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
 185 GCCTTTCTGCTCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 244
 121 TCCTGTGGCCATATGAATCATCAGATGGGTCAACAAATCAAGATCTGATGCTGTC 180
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 425 AGATAATGATCGCTTGACACCCCTTTGGATCCCAATTAAGAAATATTTTGGGGCTTAG 484
 361 CAAATTTCTTGGAAACACATCGGCTTATGGGCAACATTTTGGGCTTACTCTTTGGTTCAAT 420
 485 CAAATTTCTTGGAAACACATCGGCTTATGGGCAACATTTTGGGCTTACTCTTTGGTTCAAT 544
 421 GACAACTCTCGAACTGGAAATCCCTCTGAGGCTGTTGAAATATCCACTTGTGT 480
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 481 TTTTCTCATGCTTTGGGGCATTCAGGACATTTTATCTGCTATTGGCATTGACCTGGC 540
 605 TTTTCTCATGCTTTGGGGCATTCAGGACATTTTATCTGCTATTGGCATTGACCTGGC 664
 541 ATCTCATGCTTTATAGTTGCTGCTGATGAAACACAGATAGATCTGCACTTCAACTTA 600
 665 ATCTCATGCTTTATAGTTGCTGCTGATGAAACACAGATAGATCTGCACTTCAACTTA 724

601 CTATTTCAAGGACCAATCTGCTGCAGAAATAGGGGCAAGTCTTGGCTCTACCTTAGAAC 660
 725 CTATTTCAAGGACCAATCTGCTGCAGAAATAGGGGCAAGTCTTGGCTCTACCTTAGAAC 784
 661 CCTGAAACAAGAGGAGGAGACACATATACGAAATGAGCAGGTACGCAAGAGCAAAAGA 720
 785 CCTGAAACAAGAGGAGGAGACACATATACGAAATGAGCAGGTACGCAAGAGCAAAAGA 844
 721 ATGTTCCCAAGCTCTCAGTCTGATTTTTCGACATTTGATGCAATGCAATGCAATGCAATG 780
 845 ATGTTCCCAAGCTCTCAGTCTGATTTTTCGACATTTGATGCAATGCAATGCAATGCAATG 904
 781 ATTAGATTTAAAGTTTGAATGGAACAACCTGGAAGGACTCTATTGATAGGCAAAATATAGC 840
 905 ATTAGATTTAAAGTTTGAATGGAACAACCTGGAAGGACTCTATTGATAGGCAAAATATAGC 964
 841 AGTAATGGAACATCTTTTGGTGGAGCAACGGTTATTCAGACTCTTTAGTAGGAAGATCAGAG 900
 965 AGTAATGGAACATCTTTTGGTGGAGCAACGGTTATTCAGACTCTTTAGTAGGAAGATCAGAG 1024
 901 ATTCAAGATGTTGATTTGCTGCTGATGCAATGCAATGCAATGCAATGCAATGCAATGCAAT 960
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 1085 CAGAATTTCTCAGCCCTCTTTTATCAACTCTGCAATATTTTCCCAATATCTCTGCTAATAT 1144
 1021 CATATAAATGAAATAATGCTACTACCTGATTAAGAAAGAAAGATGATTAATCAATCAGGGG 1080
 1145 CATATAAATGAAATAATGCTACTACCTGATTAAGAAAGAAAGATGATTAATCAATCAGGGG 1204
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 1321 CATCATGTTTACAGAACTCTTTCAGGAATAGAGAAATACAAAT 1361
 1445 CATCATGTTTACAGAACTCTTTCAGGAATAGAGAAATACAAAT 1485

RESULT 6
 US-08-318-905-7
 ; Sequence 7, Application US/08318905
 ; Patent No. 5641669
 ; GENERAL INFORMATION:
 ; APPLICANT: Cousens, Lawrence S.
 ; APPLICANT: Eberhardt, Christine D.
 ; APPLICANT: Gray, Patrick W.
 ; APPLICANT: Le Trong, Hai
 ; APPLICANT: Tjoelker, Larry W.
 ; APPLICANT: Wilder, Cheryl L.
 ; TITLE OF INVENTION: Platelet-Activating Factor Acetyl
 ; NUMBER OF SEQUENCES: 26
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Marshall, O'Toole, Gertein, Murray & Borun
 ; STREET: 6300 Sears Tower, 233 South Wacker Drive
 ; CITY: Chicago
 ; STATE: Illinois

```

COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/318,905
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
PRIORITY NUMBER: US 08/133,803
FILING DATE: 6-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: No. 5641669and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 32205
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3658
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1520 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 162..1484
US-08-318-905-7

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Query Match	99.9%;	Score 1359.4;	DB 1;	Length 1520;
Best Local Similarity	99.9%;	Pred. No. 0;		
Matches 1360;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
Qy	1	TGAGAGACTAAGCTGAAACTGCTGCTCAGCTCCCAAGATGGTGCACCCCAAAATGGCATG	60	
Db	125	TGAGAGACTAAGCTGAAACTGCTGCTCAGCTCCCAAGATGGTGCACCCCAAAATGGCATG	184	
Qy	61	GCITTTTCTGCTCTGCGGCTGCCTGGCTGTGGTTTATCCTTTTGACGTGGCAATACATAAA	120	
Db	185	GCITTTTCTGCTCTGCGGCTGCCTGGCTGTGGTTTATCCTTTTGACGTGGCAATACATAAA	244	
Qy	121	TCCTGTGGCCATATGAAATCATCAGCATGGGTCAACAAATACAAATCTGATGGGTGC	180	
Db	245	TCCTGTGGCCATATGAAATCATCAGCATGGGTCAACAAATACAAATCTGATGGGTGC	304	
Qy	181	TGCAAGCTTTGGCCAAACTAAATCCCCCGGGGAAATGGGCCCTTATTCCTGTGGTGTAC	240	
Db	305	TGCAAGCTTTGGCCAAACTAAATCCCCCGGGGAAATGGGCCCTTATTCCTGTGGTGTAC	364	
Qy	241	AGACTTAATGTTTGATCACACTAATAAGGGCACCTTCTTGCGTTTATATTATTCATCCCA	300	
Db	365	AGACTTAATGTTTGATCACACTAATAAGGGCACCTTCTTGCGTTTATATTATTCATCCCA	424	
Qy	301	AGATAATGATCGCCTTGACACCCCTTTGGATCCCAATAAAGATATTTTTGGGGTCTTAG	360	
Db	425	AGATAATGATCGCCTTGACACCCCTTTGGATCCCAATAAAGATATTTTTGGGGTCTTAG	484	
Qy	361	CAAAATCTTTGGACACACTGGCTTATGGGCAACATTTTGAGGTTACTCTTTGGTTCAT	420	
Db	485	CAAAATCTTTGGACACACTGGCTTATGGGCAACATTTTGAGGTTACTCTTTGGTTCAT	544	
Qy	421	GACAACTCCTGCAAACTGGAAATCCCTCTGAGGCTGGTGAAAAATATCCACTTGTGT	480	
Db	545	GACAACTCCTGCAAACTGGAAATCCCTCTGAGGCTGGTGAAAAATATCCACTTGTGT	604	
Qy	481	TTTTTCTCATGGTCTGGGGCAATTCAGGACATTTATTCGTATTCGCAATGACCTGGC	540	
Db	605	TTTTTCTCATGGTCTGGGGCAATTCAGGACATTTATTCGTATTCGCAATGACCTGGC	664	

541	QY	ATCTCATGGGTTTATAGTTGCTGCTGTAGAACACAGAGATAGATCTGCACTCTGCAACTT	600
665	Db	ATCTCATGGGTTTATAGTTGCTGCTGTAGAACACAGAGATAGATCTGCACTCTGCAACTT	724
601	QY	CTATTTTCAAGGACCAATCTGCTGCAGAAATAGGGGCAAGCTCTTGGCTCTTACCTTAGAAC	660
725	Db	CTATTTTCAAGGACCAATCTGCTGCAGAAATAGGGGCAAGCTCTTGGCTCTTACCTTAGAAC	784
661	QY	CCTGAAACAAGAGGAGGAGACACATATACGAAATGAGCAGGTACGGCAAAAGACGCAAAAGA	720
785	Db	CCTGAAACAAGAGGAGGAGACACATATACGAAATGAGCAGGTACGGCAAAAGAGCAAAAGA	844
721	QY	ATGTTTCCCAAGCTCTCAGTCTGATTTCTTGACATTGATCATGGAAGCCAGTGAAGATGC	780
845	Db	ATGTTTCCCAAGCTCTCAGTCTGATTTCTTGACATTGATCATGGAAGCCAGTGAAGATGC	904
781	QY	ATTAGAGTTTAAAGTTTGGATTGAAACAACTGAAGGACTCTATTGATAGGGGAAAAAATAGC	840
905	Db	ATTAGAGTTTAAAGTTTGGATTGAAACAACTGAAGGACTCTATTGATAGGGGAAAAAATAGC	964
841	QY	AGTAAATTGGAACATCTTTTGGTGGAGGAAACGGTTTATTCAGACTCTTAGTGAAGATCAGAG	900
965	Db	AGTAAATTGGAACATCTTTTGGTGGAGGAAACGGTTTATTCAGACTCTTAGTGAAGATCAGAG	1024
901	QY	ATTTCAGATGTGTTATTTGCCCTGATCGATCGATGGATGTTTCCACTGGGTGATGAAGTATATTC	960
1025	Db	ATTTCAGATGTGTTATTTGCCCTGATCGATGGATGTTTCCACTGGGTGATGAAGTATATTC	1084
961	QY	CAGAAATCTCTCAGCCCTCTTTTTTTATCAACTCTGAATATTTTCCAATATCTCTGCTAATAT	1020
1085	Db	CAGAAATCTCTCAGCCCTCTTTTTTTATCAACTCTGAATATTTTCCAATATCTCTGCTAATAT	1144
1021	QY	CATAAAATGAAAAATGCTACTCACTGATTAAGAAAAAGAAAGATGATTAACAATCAGGGG	1080
1145	Db	CATAAAATGAAAAATGCTACTCACTGATTAAGAAAAAGAAAGATGATTAACAATCAGGGG	1204
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1141	QY	GCTCAAAATTTAAAGGGAGACATAGATTTCAAATGCAGCTATTGATCTTAGCAACAAAGCTTC	1200
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1201	QY	ATTAGCATTTTACAAAAGCATTTAGGACTTTCAATAAAGATTTTGTATCAGTGGGACTGCTT	1260
1325	Db	ATTAGCATTTTACAAAAGCATTTAGGACTTTCAATAAAGATTTTGTATCAGTGGGACTGCTT	1384
1261	QY	GATTTGAAGGAGATGATGAGAACTTTATTCAGGGGACCAACATTTAAACAACCAATCAACA	1320
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1321	QY	CATCATGTTTACGAACCTCTTTCAGGAATAGAGAAATACAATT	1361
1445	Db	CATCATGTTTACGAACCTCTTTCAGGAATAGAGAAATACAATT	1485

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RESULT 7
US-08-483-232-7
; Sequence 7, Application US/08483232
; Patent No. 5656431
; GENERAL INFORMATION:
; APPLICANT: Cousins, Lawrence S.
; APPLICANT: Eberhardt, Christine D.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Le Trong, Hai
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor
; TITLE OF INVENTION: Acetylhydrolase
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
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RESULT 9
US-08-485-938A-7
; Sequence 7, Application US/08485938A
; Patent No. 5847088
; GENERAL INFORMATION:
; APPLICANT: Cousins, Lawrence S.

Qy	301	AGATAATGATCGCCTTGACACCCCTTTGGATCCAAATAAAGAATATTTTTGGGTCTTAG	360
Db	425	AGATAATGATCGCCTTGACACCCCTTTGGATCCAAATAAAGAATATTTTTGGGTCTTAG	484
Qy	361	CAAAATTTCTTGGAACACACTGCGCTTATGGGCACAAATTTTGAGTTACTCTTTGGTTCAAT	420

Query Match	99.9%	Score 1359.4;	DB 1;	Length 1520;
Best Local Similarity	99.9%	Pred. No. 0;		
Matches 1360:	Conservative	0;	Mismatches	1;
			Indels	0;
			Gaps	0;

1	Qy	1	TGAGAGACTAAGCTGAAACTGCTGCTCAGCTCCCAAGATGGTGCCACCAGAAATTCGATGT	60
125	Db	125	TGAGAGACTAAGCTGAAACTGCTGCTCAGCTCCCAAGATGGTGCCACCAGAAATTCGATGT	184
61	Qy	61	GCITTTTCTGCGCTCTGCGGCTGCCTGGCTGTGTTTTATCCTTTTGACTGGCAATACATAAA	120
185	Db	185	GCITTTTCTGCGCTCTGCGGCTGCCTGGCTGTGTTTTATCCTTTTGACTGGCAATACATAAA	244
121	Qy	121	TCCTGTTGCCCATATGAATCATCAGCATGGGTCAACAAAATACAAGTACTGATGGCTGC	180
245	Db	245	TCCTGTTGCCCATATGAATCATCAGCATGGGTCAACAAAATACAAGTACTGATGGCTGC	304
181	Qy	181	TGCAAGCTTTTGGCCAAACTTAAATCCCGCGGGAAATGGCGCTTATTCGGTTGGTTGTAC	240
305	Db	305	TGCAAGCTTTTGGCCAAACTTAAATCCCGCGGGAAATGGCGCTTATTCGGTTGGTTGTAC	364
241	Qy	241	AGACTTAATGTTTGATCACACTAATAAGGGCACCTTCTTGCGTTTATATATCCCATCCCA	300
365	Db	365	AGACTTAATGTTTGATCACACTAATAAGGGCACCTTCTTGCGTTTATATATCCCATCCCA	424
301	Qy	301	AGATAATGATCGCCTTGACACCCCTTTGGATCCCAATAAAGAATATTTTTTGGGGCTCTTAG	360
425	Db	425	AGATAATGATCGCCTTGACACCCCTTTGGATCCCAATAAAGAATATTTTTTGGGGCTCTTAG	484
361	Qy	361	CAAAATTTCTTGGAAACACACTGCTTTATGGGCACAACTTTTGGGTTACTCTTTGGTTCAAT	420

Db 1325 ATTAGCATTTACAAAGCAITTTAGGACTTCATAAGATTTTGTATCAGTGGGACTGCTT 1384
QY 1261 GATTGAAGAGATGATGAGATCTTATTCAGGGACCAACATTTAAACACCAACCAATCAACA 1320
Db 1385 GATTGAAGAGATGATGAGATCTTATTCAGGGACCAACATTTAAACACCAACCAATCAACA 1444
QY 1321 CATCATGTTACAGAACTCTTCAGGAATAGAGAAATACAATT 1361
Db 1445 CATCATGTTACAGAACTCTTCAGGAATAGAGAAATACAATT 1485

RESULT 11
US-09-328-474-7
; Sequence 7, Application US/09328474
; Patent No. 6045794
; GENERAL INFORMATION:
; APPLICANT: Cousens, Lawrence S.
; APPLICANT: Eberhardt, Christine D.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Le Trong, Hai
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor
; TITLE OF INVENTION: Acetylhydrolase
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/328,474
; FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/483,232
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/318,905
FILING DATE: 06-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,803
FILING DATE: 06-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Rin-Laures, Li-Hsien
REGISTRATION NUMBER: 33,547
REFERENCE/DOCKET NUMBER: 27866/34026
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3658

INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1520 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
FEATURE:
NAME/KEY: CDS
LOCATION: 162..1484
US-09-328-474-7

Query Match 99.9%; Score 1359.4; DB 3; Length 1520;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1360; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGAGAGACTTAAGCTGAAATCTGCTGCTCAGCTCCCAAGATGCTGCCAACCACAAATTCATGT 60
Db 125 TGAGAGACTTAAGCTGAAATCTGCTGCTCAGCTCCCAAGATGCTGCCAACCACAAATTCATGT 184
QY 61 GCTTTTCTGCTCTCGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
Db 185 GCTTTTCTGCTCTCGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 244
QY 121 TCCTGTTGCCCATATGAATCATCAGCATGGTCAACAAATACAAATACAAATACAAATACAAATACAA 180
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QY 241 AGACTTAATGTTTGTATCAGCTTAATAAGGGACCTTCTTGGCTTATATATATATATATATATATAT 300
Db 365 AGACTTAATGTTTGTATCAGCTTAATAAGGGACCTTCTTGGCTTATATATATATATATATATATAT 424
QY 301 AGATAATGATCGCTTGGACACCTTTGGATCCCAATAAAGAAATATTTTGGGGTCTTAG 360
Db 425 AGATAATGATCGCTTGGACACCTTTGGATCCCAATAAAGAAATATTTTGGGGTCTTAG 484
QY 361 CAAATTTCTTGGAAACACACTGGCTTATGGGCAACATTTTGGAGTTTACTCTTTGGTTCAT 420
Db 485 CAAATTTCTTGGAAACACACTGGCTTATGGGCAACATTTTGGAGTTTACTCTTTGGTTCAT 544
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Db 545 GACAACTCTGCAAACTGGAATCCCTCTGAGGCTTGGTGAAGAAATATCCACTTGTGT 604
QY 481 TTTTCTCATGCTCTTGGGGCACTTATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540
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QY 541 ATCTCATGCTTATAGTTGCTGCTGTAGAACACAGAGATAGATCTGCACTCTGCAACTT 600
Db 665 ATCTCATGCTTATAGTTGCTGCTGTAGAACACAGAGATAGATCTGCACTCTGCAACTT 724
QY 601 CTATTTCAAGGACCAATCTGCTGCAAGATAGGGCAAGTCTTGGCTCTACCTTAGAAC 660
Db 725 CTATTTCAAGGACCAATCTGCTGCAAGATAGGGCAAGTCTTGGCTCTACCTTAGAAC 784
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Db 785 CCTGAAACAAGAGAGAGAGACACATATAGCAATGAGCAGGTACGCAAGAGCAAGAA 844
QY 721 ATGTTCCCAAGCTCTCAGTCTGATTTTGCATTTGATCATGGAAGCCAGTGAAGATGC 780
Db 845 ATGTTCCCAAGCTCTCAGTCTGATTTTGCATTTGATCATGGAAGCCAGTGAAGATGC 904
QY 781 ATTAGATTTAAAGTTTGTATGGAACAACTGAAGGACTTATTTGATAGGGAAGAAATAGC 840
Db 905 ATTAGATTTAAAGTTTGTATGGAACAACTGAAGGACTTATTTGATAGGGAAGAAATAGC 964
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QY 901 ATTACATGTTGGTATTTGCCCTTGGATCGATGGATGTTTCCACTGGGTGATGAAGTATATTC 960
Db 1025 ATTACATGTTGGTATTTGCCCTTGGATCGATGGATGTTTCCACTGGGTGATGAAGTATATTC 1084
QY 961 CAGAAATCTCAGCCCTCTTTTATCACTCTGAATATTTCCATATCTCTCTCTCTCTCTCTCTCT 1020
Db 1085 CAGAAATCTCAGCCCTCTTTTATCACTCTGAATATTTCCATATCTCTCTCTCTCTCTCTCTCT 1144
QY 1021 CATAAAAATGAAAAAATGCTACTCCTGATTAAGAAAGAAAGAGATGATTACAATCAGGGG 1080
Db 1145 CATAAAAATGAAAAAATGCTACTCCTGATTAAGAAAGAAAGAGATGATTACAATCAGGGG 1204

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Db 1265 GCTCAATTTAAAGGAGACATAGATTCAAAATGAGCTATTGATCTTAGCAACAAAGCTTC 1324
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Db 1325 ATTAGCATTTTCAAAAGCATTTAGGACTTTCATAAAGATTTTGTATGATGAGTGGAGCTGCTT 1384
QY 1261 GATTGAAGGAGATGATGAGATCTTATTCAGGAGCCCAACATTAACACACCAATCAACA 1320
Db 1385 GATTGAAGGAGATGATGAGATCTTATTCAGGAGCCCAACATTAACACACCAATCAACA 1444
QY 1321 CATCATGTTACAGAACTCTTCAGGAATAGAGAAATACAAT 1361
Db 1445 CATCATGTTACAGAACTCTTCAGGAATAGAGAAATACAAT 1485

RESULT 12

US-09-100-546-7
; Sequence 7, Application US/09100546
; Patent No. 6099836
; GENERAL INFORMATION:
; APPLICANT: Cousens, Lawrence S.
; APPLICANT: Eberhardt, Christine D.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Le Trong, Hai
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor
; TITLE OF INVENTION: Acetylhydrolase
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/100,546
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,715
; FILING DATE:
; APPLICATION NUMBER: US 08/318,905
; FILING DATE: 06-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 06-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6099836and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/32793
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3658
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1520 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 162..1484
; US-09-100-546-7
Query Match 99.9%; Score 1359.4; DB 3; Length 1520;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1360; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 TGAGAGACTAAGCTGAAACTGCTGCTCAGCTCCCAAGATGGTGCACCCCAAAATTTGCAATG 60
Db 125 TGAGAGACTAAGCTGAAACTGCTGCTCAGCTCCCAAGATGGTGCACCCCAAAATTTGCAATG 184
QY 61 GCTTTTCTGCTCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
Db 185 GCTTTTCTGCTCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 244
QY 121 TCCTGTTGCCCATATGAATCATCAGCATGGGTCAACAAATACAAATACAAATACAAATACAAAT 180
Db 245 TCCTGTTGCCCATATGAATCATCAGCATGGGTCAACAAATACAAATACAAATACAAATACAAAT 304
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Db 305 TGCAAGCTTTGGCCAAACTAAATATCCCGGGGAAATGGGCCCTTATTTCCGTTGCTGTTGATC 364
QY 241 AGACTTTAATGTTTGTATGATCACAATAAAGGACACCTTTCTTGCCTGTTTATATATATATATAT 300
Db 365 AGACTTTAATGTTTGTATGATCACAATAAAGGACACCTTTCTTGCCTGTTTATATATATATATAT 424
QY 301 AGATAATGATCGCTTGGACACCTTTGGATCCCAATTAAGAAATATTTTGGGGTCTTAG 360
Db 425 AGATAATGATCGCTTGGACACCTTTGGATCCCAATTAAGAAATATTTTGGGGTCTTAG 484
QY 361 CAAATTTCTTGGAAACACACCTGCTTATGGCAACATTTTGGAGTACTCTTTGGTTCAAT 420
Db 485 CAAATTTCTTGGAAACACACCTGCTTATGGCAACATTTTGGAGTACTCTTTGGTTCAAT 544
QY 421 GACAACTCTGCAAACTGGAATTTCCCTCTGAGGCTGTTGAAATAATATCCACTTTGTTGT 480
Db 545 GACAACTCTGCAAACTGGAATTTCCCTCTGAGGCTGTTGAAATAATATCCACTTTGTTGT 604
QY 481 TTTTCTCATGCTTTGGGGCATTTGAGACACCTTTATTCGCTATTGGGCAATGACCTGGC 540
Db 605 TTTTCTCATGCTTTGGGGCATTTGAGGACACCTTTATTCGCTATTGGGCAATGACCTGGC 664
QY 541 ATCTCATGCTTTATAGTTGCTGCTGTAGAAACACAGATAGATCTGCACTCTGCAACTTA 600
Db 665 ATCTCATGCTTTATAGTTGCTGCTGTAGAAACACAGATAGATCTGCACTCTGCAACTTA 724
QY 601 CTATTTCAAGGACCAATCTGCTGCAGAAATAGGGGCAAGTCTTGGCTCTTACCTTAGAAC 660
Db 725 CTATTTCAAGGACCAATCTGCTGCAGAAATAGGGGCAAGTCTTGGCTCTTACCTTAGAAC 784
QY 661 CCTGAACAAGAGGAGGAGACACATATACGAATGAGCAGGTACGGCAAGAGCAAGA 720
Db 785 CCTGAACAAGAGGAGGAGACACATATACGAATGAGCAGGTACGGCAAGAGCAAGA 844
QY 721 ATGTTCCCAAGCTCTCAGTCTGATTTCTGACATTTGATCTGGAAGCCAGTGAAGATGC 780
Db 845 ATGTTCCCAAGCTCTCAGTCTGATTTCTGACATTTGATCTGGAAGCCAGTGAAGATGC 904
QY 781 ATTAGATTTTAAAGTTTGATATGGAACAACCTGAAGGACTCTTATTTGATAGGAAATATAGC 840
Db 905 ATTAGATTTTAAAGTTTGATATGGAACAACCTGAAGGACTCTTATTTGATAGGAAATATAGC 964
QY 841 AGTAATTTGACATTTCTTTTGGTGGAGCAACCGTTTATTCAGACTCTTAGTGAAGATCAGAG 900
Db 965 AGTAATTTGACATTTCTTTTGGTGGAGCAACCGTTTATTCAGACTCTTAGTGAAGATCAGAG 1024
QY 901 ATTACATGTTGGTATTGCTTCCATGATCATGATGTTTCCACTGGGTGATCAAGTATATTC 960
Db 1025 ATTACATGTTGGTATTGCTTCCATGATCATGATGTTTCCACTGGGTGATCAAGTATATTC 1084

QY 961 CAGAATTCCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAAATATCTCTTAATAT 1020
Db 1085 CAGAATTCCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAAATATCTCTTAATAT 1144
QY 1021 CATAAATGAAATAATGCTACTCAGCTGATAAGAAAGAAAGATGATTACAATCAGGGG 1080
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Db 1205 TTCAGTCCACCAATTTGCTGACTTCACTTTTGCACCTGGCAAAATTAATTGGACACAT 1264
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QY 1261 GATTGAAGGAGATGATGAGATCTTATTCAGGGACCAACATTAACACACCAATCAACA 1320
Db 1385 GATTGAAGGAGATGATGAGATCTTATTCAGGGACCAACATTAACACACCAATCAACA 1444
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Db 1445 CATCATGTTACAGAACTCTTCAGGAATAGAGAAATACAATT 1485

RESULT 13

US-09-010-715-7
Sequence 7, Application US/09010715
Patent No. 6146625
GENERAL INFORMATION:
APPLICANT: Cousens, Lawrence S.
APPLICANT: Eberhardt, Christine D.
APPLICANT: Gray, Patrick W.
APPLICANT: Le Trong, Hai
APPLICANT: Tjoelker, Larry W.
APPLICANT: Wilder, Cheryl L.
TITLE OF INVENTION: Platelet-Activating Factor
TITLE OF INVENTION: Acetylhydrolase
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,715
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/318,905
FILING DATE: 06-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,803
FILING DATE: 06-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: No. 6146625and, Greta B.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/32793
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448

TELEX: 25-3658
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1520 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 162...1484
US-09-010-715-7

Query Match 99.9%; Score 1359.4; DB 3; Length 1520;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1360; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 TGAGAGACTAAGCTGAACTGCTGCTCAGCTCCAGATGGTGGCCACCCAAATTCATGT 60
Db 125 TGAGAGACTAAGCTGAACTGCTGCTCAGCTCCAGATGGTGGCCACCCAAATTCATGT 184
QY 61 GCTTTTCTGCTCTCGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
Db 185 GCTTTTCTGCTCTCGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 244
QY 121 TCCTGTTGCCATATGAATCATCAGCATGGTCAACAAAATACAAGTACTGATGCTGC 180
Db 245 TCCTGTTGCCATATGAATCATCAGCATGGTCAACAAAATACAAGTACTGATGCTGC 304
QY 181 TGAAGCTTTGGCCAAATCAAAAATCCCGGGGAAATGGGCTTATTCGTTGGTTGTAC 240
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QY 241 AGACTTAATGTTGATCACACTAAAGGGACCTTCTTTCGCTGCTTATATATTCATCCCA 300
Db 365 AGACTTAATGTTGATCACACTAAAGGGACCTTCTTTCGCTGCTTATATATTCATCCCA 424
QY 301 AGATAATGATCGCTTTGACACACCTTTGGATCCCAATAAAGAAATATTTTGGGGCTTAG 360
Db 425 AGATAATGATCGCTTTGACACACCTTTGGATCCCAATAAAGAAATATTTTGGGGCTTAG 484
QY 361 CAAATTTCTTGAACACACTGCTTATGGGCAACATTTTGGAGTACTCTTTGGTTCAAT 420
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Db 545 GACAACTCTGCAAACTGGAATTCCTCTGAGGCTGGTGAATAATATCCACTTGTGT 604
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Db 781 TCTATTGATAGGGAAAAAANTAGCAAGTAATGGACAATCTTTTGGTGAGCAACGGTTATT 840
Qy 878 CAGACTCTTAGTGAAGATCAGAGATTCAGATGTGTTATGGCCCTGGATGATGATGTTT 937
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Qy 1058 AGAAGATGATTACAATCAGGGTTTCAGTCCACCAGAAATTTGCTGACTTCACCTTTGCA 1117
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Qy 1178 ATTGATCTTAGCAACAAGCTTCATTAGCAATCTTACAAAAGCAATTTAGGACTTCATAAA 1237
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Db 1201 GATTTTGATCAGTGGGACTGCTTGATTGAAGGAGATGATGAGATCTTATTCAGGGACC 1260
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Qy 1358 AATT 1361
Db 1321 AATT 1324
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 15, 2005, 16:15:21 ; Search time 1326.88 Seconds
(without alignments)
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Title: US-09-922-067F-9

Perfect score: 1361

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 5544816 seqs, 2976611598 residues

Total number of hits satisfying chosen parameters: 11089632

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1361	100.0	1361	9	US-09-922-067-9
2	1361	100.0	1361	15	US-10-173-233-9
3	1361	100.0	1361	16	US-10-406-156-9
4	1361	100.0	1561	9	US-09-962-832-110
5	1359.4	99.9	1505	17	US-10-172-118-1120
6	1359.4	99.9	1505	17	US-10-342-887-1120
7	1359.4	99.9	1505	18	US-10-755-889-277
8	1359.4	99.9	1520	9	US-09-729-402-7
9	1359.4	99.9	1520	14	US-10-003-978A-7
10	1358.6	99.8	1964	18	US-10-741-601-90
11	1355.6	99.6	1845	18	US-10-741-601-89
					Sequence 9, Appli
					Sequence 9, Appli
					Sequence 110, App
					Sequence 1120, Ap
					Sequence 1120, Ap
					Sequence 277, App
					Sequence 7, Appli
					Sequence 7, Appli
					Sequence 90, Appl
					Sequence 89, Appl

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13	1162.4	85.4	1335	9	US-09-729-402-30	Sequence 30, Appl
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15	1049.6	77.1	1533	9	US-09-729-402-23	Sequence 23, Appl
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40	238.6	17.5	385	9	US-09-962-832-58	Sequence 58, Appl
41	238.6	17.5	385	9	US-09-880-107-1974	Sequence 1974, Ap
42	238.6	17.5	385	11	US-09-968-007A-185	Sequence 185, App
43	234.6	17.2	437	9	US-09-960-352-10049	Sequence 10049, A
44	234.6	17.2	441	10	US-09-918-995-13782	Sequence 13782, A
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ALIGNMENTS

RESULT 1

US-09-922-067-9

; Sequence 9, Application US/09922067

; Patent No. US20020177209A1

; GENERAL INFORMATION:

; APPLICANT: MacPhee, Colin Houston

; Tew, David Graham

; Southan, Christopher Donald

; Hickey, Dierdre Mary Bernadette

; Gloger, Israel Simon

; Lawrence, Geoffrey Mark Prouse

; Rice, Simon Quentyn John

; TITLE OF INVENTION: Lipoprotein Associated Phospholipase A2, Inhibitors
Thereof And Use Of The Same In Diagnosis And Therapy

; NUMBER OF SEQUENCES: 11

; CORRESPONDENCE ADDRESSES:

; ADDRESSEE: Smithkline Beecham Corporation

; STREET: 709 Swedeland Road

; CITY: King of Prussia

; STATE: PA

; COUNTRY: USA

; ZIP: 19406

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/922.067

; FILING DATE: 03-Aug-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/193,130

; FILING DATE: 1998-11-17

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLIATION NUMBER: US/10/173,233
FILING DATE: 14-Jun-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/569,899
FILING DATE: 12-May-2000
ATTORNEY/AGENT INFORMATION:
NAME: Dustman, Wayne J.
REGISTRATION NUMBER: 33,870
REFERENCE/DOCKET NUMBER: P30693
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5023
TELEFAX: 610-270-5090
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1361 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 38..1360
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-173-233-9

Query Match 100.0%; Score 1361; DB 15; Length 1361;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1361; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3
US-10-406-156-9
; Sequence 9, Application US/10406156
; Publication No. US20030186421A1
; GENERAL INFORMATION:
; APPLICANT: MacPhee, Colin Houston
; Tew, David Graham
; Southan, Christopher Donald
; Hickey, Dierdre Mary Bernadette
; Gloger, Israel Simon
; Lawrence, Geoffrey Mark Prouse
; Rice, Simon Quentyn John
; TITLE OF INVENTION: Compounds
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road

CITY: King of Prussia
 STATE: PA
 COUNTRY: USA
 ZIP: 19406
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25 (BPO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/406,156
 FILING DATE: 02-Apr-2003
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09/569,899
 FILING DATE: 12-May-2000
 APPLICATION NUMBER: 09/294,384
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Dustman, Wayne J.
 REGISTRATION NUMBER: 33,870
 REFERENCE/DOCKET NUMBER: P30693
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 610-270-5023
 TELEFAX: 610-270-5090
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1361 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 38..1360
 SEQUENCE DESCRIPTION: SEQ ID NO: 9:
 US-10-406-156-9

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 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1361; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 4

US-09-962-832-110
 ; Sequence 110, Application US/09962832
 ; Patent No. US20020110821A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ebner, Reinhard
 ; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signal
 ; TITLE OF INVENTION: Sets

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; FILE REFERENCE: 689290-74
; CURRENT APPLICATION NUMBER: US/09/962,832
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US/60/235,077
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,280
; PRIOR FILING DATE: 2000-09-25
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 110
; LENGTH: 1561
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-962-832-110

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Query Match      100.0%; Score 1361; DB 9; Length 1561;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1361; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 240 GCTTTCTGCTCTGCGGCTGCCCTGGCTGTGTTTATCTTTTACCTGGCAATACATAAA 299
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Qy 1261 GATTGAGGAGATGATGAGATCTTATTCAGGGGACCAACATTAACCAACCAATCAACA 1320
Db 1440 GATTGAGGAGATGATGAGATCTTATTCAGGGGACCAACATTAACCAACCAATCAACA 1499
Qy 1321 CATCATGTTACAGAACTCTTCAGGAATAGAGAAATACAATT 1361
Db 1500 CATCATGTTACAGAACTCTTCAGGAATAGAGAAATACAATT 1540

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RESULT 5

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US-10-172-118-1120
; Sequence 1120, Application US/10172118
; Publication No. US20030224374A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Chris
; APPLICANT: Van 't Veer, Laura
; APPLICANT: Van de Vijver, Marc
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9101-175-999
; CURRENT APPLICATION NUMBER: US/10/172,118
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/380,770
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 1120
; LENGTH: 1505
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NM_005084
; DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-1120

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Query Match      99.9%; Score 1359.4; DB 17; Length 1505;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1360; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 TGAGAGACTAAGCTGAACCTGCTGCTCAGCTCCCAAGATGGTGGCCCAAAATTCATGT 60

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Db 425 AGATPATGATCGCCCTTGACACCCCTTTGGATCCCAATAAAGAAATATTTTGGGGCTCTTAG 484
Qy 361 CAAATTTCTTGGAAACACACTGGCTTATGGGCAACATTTTGAGGTTACTCTTTGGTTCAAT 420
Db 485 CAAATTTCTTGGAAACACACTGGCTTATGGGCAACATTTTGAGGTTACTCTTTGGTTCAAT 544
Qy 421 GACAACTCTGCAAACTGGAAATCCCTCTGAGGCCCTGGTGAAATAATCCACTTTGTGT 480
Db 545 GACAACTCTGCAAACTGGAAATCCCTCTGAGGCCCTGGTGAAATAATCCACTTTGTGT 604
Qy 481 TTTTCTCATGCTCTGGGGCAATTCAGACACTTTTATCTGCTATTCGCTATTCGCAATTCACCTGGC 540
Db 605 TTTTCTCATGCTCTGGGGCAATTCAGACACTTTTATCTGCTATTCGCTATTCGCAATTCACCTGGC 664
Qy 541 ATCTCATGGGTTATAGTTGCTGCTAGAACACAGAGATAGATCTGCATCTGCAACTTA 600
Db 665 ATCTCATGGGTTATAGTTGCTGCTAGAACACAGAGATAGATCTGCATCTGCAACTTA 724
Qy 601 CTATTTCAAGGACCAATCTGCTGAGAAATAGGGGCAAGTCTTTGGCTCTACCTTAGAAC 660
Db 725 CTATTTCAAGGACCAATCTGCTGAGAAATAGGGGCAAGTCTTTGGCTCTACCTTAGAAC 784
Qy 661 CCTGAACAAGAGGAGGAGACACATATACGAATGAGCAGTACGGCAAGAGCAAGA 720
Db 785 CCTGAACAAGAGGAGGAGACACATATACGAATGAGCAGTACGGCAAGAGCAAGA 844
Qy 721 ATGTTCCCAAGCTCTCAGTCTGATTTCTTGACATTTGATCGAAGCCAGTGAAGATGC 780
Db 845 ATGTTCCCAAGCTCTCAGTCTGATTTCTTGACATTTGATCGAAGCCAGTGAAGATGC 904
Qy 781 ATTAGATTTAAAGTTGATTTGGAACAACTGAAGGACTCTATTGATAGGGGAAATAATGAC 840
Db 905 ATTAGATTTAAAGTTGATTTGGAACAACTGAAGGACTCTATTGATAGGGGAAATAATGAC 964
Qy 841 AGTAATTTGGACATTTCTTTGGTGAGCAACGGTTATTCAGACTCTTATGAGAGATCAGAG 900
Db 965 AGTAATTTGGACATTTCTTTGGTGAGCAACGGTTATTCAGACTCTTATGAGAGATCAGAG 1024
Qy 901 ATTCAGATGTGGTATTTGCCCTTGATGATGATGATTTTCCACTGGGTGATGAAGTATATTC 960
Db 1025 ATTCAGATGTGGTATTTGCCCTTGATGATGATGATTTTCCACTGGGTGATGAAGTATATTC 1084
Qy 961 CAGAAATTCCTCAGCCCTCTTTTATCAACTCTGAATATTTTCCAAATCTCTGCTAATAT 1020
Db 1085 CAGAAATTCCTCAGCCCTCTTTTATCAACTCTGAATATTTTCCAAATCTCTGCTAATAT 1144
Qy 1021 CATTAATAATGAATAATGCTACTCACCTGATTAAGAAAGAAAGATGATTACATCAGGG 1080
Db 1145 CATTAATAATGAATAATGCTACTCACCTGATTAAGAAAGAAAGATGATTACATCAGGG 1204
Qy 1081 TTCAGTCCACAGAAATTTGCTGACTTCACTTTTGGCACTGGCAAAATAATTTGACACAT 1140
Db 1205 TTCAGTCCACAGAAATTTGCTGACTTCACTTTTGGCACTGGCAAAATAATTTGACACAT 1264
Qy 1141 GCTCAAAATTAAGGAGACATAGATTCAAATGCAAGCTTATGATCTTAGCAACAAAGCTTC 1200
Db 1265 GCTCAAAATTAAGGAGACATAGATTCAAATGCAAGCTTATGATCTTAGCAACAAAGCTTC 1324
Qy 1201 ATTAGCATTTCTTACAAAGCAATTTAGGACTTCATTAAGATTTTTCAGTGGGACTGCTT 1260
Db 1325 ATTAGCATTTCTTACAAAGCAATTTAGGACTTCATTAAGATTTTTCAGTGGGACTGCTT 1384
Qy 1261 GATTGAAGGAGATGATGAGATCTTATTCAGGGGACCAACATTAACCAACCAATCAACA 1320
Db 1385 GATTGAAGGAGATGATGAGATCTTATTCAGGGGACCAACATTAACCAACCAATCAACA 1444
Qy 1321 CATCATGTTACAGAACTCTTTCAGGAATAGAGAAATACAAT 1361
Db 1445 CATCATGTTACAGAACTCTTTCAGGAATAGAGAAATACAAT 1485
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RESULT 7

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US-10-755-889-277
; Sequence 277, Application US/10755889
; Publication No. US20040171823A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-kB
; TITLE OF INVENTION: PATHWAY
; FILE REFERENCE: D0284 NP
; CURRENT APPLICATION NUMBER: US/10755,889
; CURRENT FILING DATE: 2004-01-13
; PRIOR APPLICATION NUMBER: U.S. 60/440,068
; PRIOR FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: U.S. 60/469,757
; PRIOR FILING DATE: 2003-05-12
; NUMBER OF SEQ ID NOS: 823
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 277
; LENGTH: 1505
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-755-889-277
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Query Match 99.9%; Score 1359.4; DB 18; Length 1505;
Best Local Similarity 99.9%; Pred.No. 0;
Matches 1360; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy 1 TGAGAGACTAAGCTGAAACTGCTCTCAGCTCCCAAGATGGTGCCCAAAATTCATGT 60
Db 125 TGAGAGACTAAGCTGAAACTGCTCTCAGCTCCCAAGATGGTGCCCAAAATTCATGT 184
Qy 61 GCTTTTCTGCTCTGGGCTGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 120
Db 185 GCTTTTCTGCTCTGGGCTGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 244
Qy 121 TCCTGTTGCCCATATGAATCATCAGCATGGGTCAACAAATCAAGTACTGATGGCTGC 180
Db 245 TCCTGTTGCCCATATGAATCATCAGCATGGGTCAACAAATCAAGTACTGATGGCTGC 304
Qy 181 TGCAAGCTTTGGCCAAACTAAATCCCGGGGAAATGGGCTTTATTCGGTGGTGTGAC 240
Db 305 TGCAAGCTTTGGCCAAACTAAATCCCGGGGAAATGGGCTTTATTCGGTGGTGTGAC 364
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Db 365 AGACTTAATGTTTGATCACAATAAGGGACCTCTCTGGTGGTGGTGGTGGTGGTGGTGG 424
Qy 301 AGATAATGATCGCTTGACACCCCTTTGGATCCCAATAAAGAAATATTTTGGGGCTCTTAG 360
Db 425 AGATAATGATCGCTTGACACCCCTTTGGATCCCAATAAAGAAATATTTTGGGGCTCTTAG 484
Qy 361 CAAATTTCTTGGAAACACACTGGCTTATGGGCAACATTTTGAGGTTACTCTTTGGTTCAAT 420
Db 485 CAAATTTCTTGGAAACACACTGGCTTATGGGCAACATTTTGAGGTTACTCTTTGGTTCAAT 544
Qy 421 GACAACTCTGCAAACTGGAAATCCCTCTGAGGCCCTGGTGAAATAATCCACTTTGTGT 480
Db 545 GACAACTCTGCAAACTGGAAATCCCTCTGAGGCCCTGGTGAAATAATCCACTTTGTGT 604
Qy 481 TTTTCTCATGCTCTGGGGCAATTCAGGACACTTTTATCTGCTATTCGCTATTCGCAATTCACCTGGC 540
Db 605 TTTTCTCATGCTCTGGGGCAATTCAGGACACTTTTATCTGCTATTCGCTATTCGCAATTCACCTGGC 664
Qy 541 ATCTCATGGGTTATAGTTGCTGCTAGAACACAGAGATAGATCTGCATCTGCAACTTA 600
Db 665 ATCTCATGGGTTATAGTTGCTGCTAGAACACAGAGATAGATCTGCATCTGCAACTTA 724
Qy 601 CTATTTCAAGGACCAATCTGCTGAGAAATAGGGGCAAGTCTTTGGCTCTACCTTAGAAC 660
Db 725 CTATTTCAAGGACCAATCTGCTGAGAAATAGGGGCAAGTCTTTGGCTCTACCTTAGAAC 784
Qy 661 CCTGAACAAGAGGAGGAGACACATATACGAATGAGCAGTACGGCAAGAGCAAGA 720
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Db 785 CCTGAAACAGAGAGAGAGACATATACGAAATGACGAGTACGGCAAGAGCAAAAGA 844
Qy 721 ATGTTCCCAAGCTCTCAGTCTGATTTCTGACATTCATGCAAGCCAGTGAAGATGC 780
Db 845 ATGTTCCCAAGCTCTCAGTCTGATTTCTGACATTCATGCAAGCCAGTGAAGATGC 904
Qy 781 ATTAGATTTAAAGTTTGATATGGAACCACTGAAGGACTCTATTGATAGGGGAAAAATAGC 840
Db 905 ATTAGATTTAAAGTTTGATATGGAACCACTGAAGGACTCTATTGATAGGGGAAAAATAGC 964
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Db 1085 CAGAAATTCCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAAATATCTGCTAATAT 1144
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Qy 1321 CATCATGTTACAGAACTCTTCAGGAATAGAGAAATACAAAT 1361
Db 1445 CATCATGTTACAGAACTCTTCAGGAATAGAGAAATACAAAT 1485

RESULT 8

US-09-729-402-7

Sequence 7, Application US/09729402

Patent No. US20010021379A1

GENERAL INFORMATION:

APPLICANT: Coubens, Lawrence S.

Eberhardt, Christine D.

Gray, Patrick W.

Le Trong, Hai

Tjoelker, Larry W.

Wildner, Cheryl L.

STATE: Illinois

COUNTRY: United States of America

ZIP: 60606-6402

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

TITLE OF INVENTION: Platelet-Activating Factor

Acetylhydrolase

NUMBER OF SEQUENCES: 30

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

STREET: 6300 Sears Tower, 233 South Wacker Drive

CITY: Chicago

STATE: Illinois

COUNTRY: United States of America

ZIP: 60606-6402

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/729,402
FILING DATE: 04-Dec-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/318,905
FILING DATE: 06-OCT-1994
APPLICATION NUMBER: US 08/133,803
FILING DATE: 06-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: No. US20010021379A1and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/32793
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3658
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1520 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 162..1484
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-729-402-7

Query Match 99.9%; Score 1359.4; DB 9; Length 1520;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1360; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 TGAGAGACTAAGCTGAACCTGCTCAGCTCCCAAGATGCTGCCCAACAAATTCATGT 60
Db 125 TGAGAGACTAAGCTGAACCTGCTCAGCTCCCAAGATGCTGCCCAACAAATTCATGT 184
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Db 305 TGCAAGCTTTGGCCAAACTAAATCCCGGGGAAATGGCCCTTATTCGTTGGTTGTAC 364
Qy 241 AGACTTAATGTTTGATCACAATAAAGGCGACCTTCTTCGCTTATATATATCCATCCCA 300
Db 365 AGACTTAATGTTTGATCACAATAAAGGCGACCTTCTTCGCTTATATATATCCATCCCA 424
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Qy 361 CAAATTTCTTGGAAACACACTGGCTTATGGCAACATTTTGGAGTTACTCTTTTGGTTCAAT 420
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Qy 421 GACAACTCTGCAAACTGGAATTCCTCTCGAGGCTGGTGAATAATATCCACTTGTGT 480
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Db 605 TTTTCTCTGATGCTTTGGGGCATTCAGGACACTTTTATCTGCTTATTTGGCATTCAGCTGGC 664
Qy 541 ATCTCATGGGTTTATAGTTGCTGCTAGAAACACAGAGATAGATCTGCACTCTGCAACTTA 600
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QY 601 CTATTTCAAGGACCAATCTGCTCAGAAATAGGGGCAAGCTCTGGCTCTACCTTAGAAC 660
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QY 725 CTATTTCAAGGACCAATCTGCTCAGAAATAGGGGCAAGCTCTGGCTCTACCTTAGAAC 784
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QY 661 CCTGAAACAAGAGGAGAGACACATATACAAATAGCAGGTACGGCAAGAGCAAAAGA 720
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QY 785 CCTGAAACAAGAGGAGAGACACATATACAAATAGCAGGTACGGCAAGAGCAAAAGA 844
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QY 721 ATGTTCCCAAGCTCTCAGTCTGATCTTGTGACATTTGATGATGATGATGATGATGATG 780
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QY 845 ATGTTCCCAAGCTCTCAGTCTGATCTTGTGACATTTGATGATGATGATGATGATGATG 904
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QY 905 ATTAGATTTAAAGTTTATGATATGAACTGAGGACTCTATTGATAGGGAATATAGC 964
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QY 841 AGTAATTTGACATCTCTTTGGTGAGCAACGGTTTATTCAGACTCTTAGTGAAGATCAGAG 900
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QY 965 AGTAATTTGACATCTCTTTGGTGAGCAACGGTTTATTCAGACTCTTAGTGAAGATCAGAG 1024
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QY 901 ATTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 960
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QY 1025 ATTCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1084
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QY 961 CAGAAATCTCAGCCCTCTTTTATCACTCTGATATTTTCAATATCTCTGCTATAT 1020
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QY 1085 CAGAAATCTCAGCCCTCTTTTATCACTCTGATATTTTCAATATCTCTGCTATAT 1144
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QY 1021 CATAAAAATGAAAAATGCTACTCACCTGATAAAGAAAGATGATTAACAATCAGGGG 1080
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QY 1145 CATAAAAATGAAAAATGCTACTCACCTGATAAAGAAAGATGATTAACAATCAGGGG 1204
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QY 1081 TTCAAGTCCACAGAAATTTGCTGACTCTCTTTGCAACTGCGCAAAATTAATGGACACAT 1140
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QY 1205 TTCAAGTCCACAGAAATTTGCTGACTCTCTTTGCAACTGCGCAAAATTAATGGACACAT 1264
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QY 1141 GCTCAAAATTAAGGGAGACATAGATTTCAAAATGAGCTATTGATCTTAGCAACAAAGCTTC 1200
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QY 1265 GCTCAAAATTAAGGGAGACATAGATTTCAAAATGAGCTATTGATCTTAGCAACAAAGCTTC 1324
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QY 1261 GATTAAGGAGATGATGAGAAATCTTTATTCAGGGACCAACATTAACACCAATCAACA 1320
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QY 1385 GATTAAGGAGATGATGAGAAATCTTTATTCAGGGACCAACATTAACACCAATCAACA 1444
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QY 1321 CATCATGTTACAGAACTCTCAGAAATAGAGAAATACAATT 1361
Db |||||
QY 1445 CATCATGTTACAGAACTCTTTCAGAAATAGAGAAATACAATT 1485
Db |||||

RESULT 9
US-10-003-978A-7
; Sequence 7, Application US/10003978A
; Publication No. US20030072747A1
; GENERAL INFORMATION:
; APPLICANT: Cousins, Lawrence S.
; Eberhardt, Christine D.
; Gray, Patrick W.
; Le Trong, Hai
; Tjoelker, Larry W.
; Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall,
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois

COUNTRY: United States of America
ZIP: 60606-6357
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/003,978A
FILING DATE: 23-Oct-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/729,402
FILING DATE: 04-DEC-2000
APPLICATION NUMBER: US 09/577,758
FILING DATE: 23-MAY-2000
APPLICATION NUMBER: US 09/010,715
FILING DATE: 22-JAN-1998
APPLICATION NUMBER: US 08/480,658
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/318,905
FILING DATE: 06-OCT-1994
APPLICATION NUMBER: US 08/133,803
FILING DATE: 06-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: NO. US20030072747A1and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/37792
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1520 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 162..1484
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-003-978A-7

Query Match 99.9%; Score 1359.4; DB 14; Length 1520;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1360; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 TGAGAGACTAAGCTGAAGCTGCTGCTCAGCTCCCAAGATGGTCCACCAAAATTCATGT 60
Db 125 TGAGAGACTAAGCTGAAGCTGCTGCTCAGCTCCCAAGATGGTCCACCAAAATTCATGT 184
QY 61 GCTTTTCTGCTCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
Db 185 GCTTTTCTGCTCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 244
QY 121 TCCTGTTGCCCATATGAAATCATCAGCATGGGTCAACAAATAACAAGTACTGATGCTGC 180
Db 245 TCCTGTTGCCCATATGAAATCATCAGCATGGGTCAACAAATAACAAGTACTGATGCTGC 304
QY 181 TGCAAGCTTTGGCCAAACTAAATATCCCGGGGAAATGGCCCTATTCGTTGGTTGATC 240
Db 305 TGCAAGCTTTGGCCAAACTAAATATCCCGGGGAAATGGCCCTATTCGTTGGTTGATC 364
QY 241 AGACTTAATGTTTGTATCAGACTAATAAGGACCTCTTTCGCTTTATATTATTCATCCCA 300
Db 365 AGACTTAATGTTTGTATCAGACTAATAAGGACCTCTTTCGCTTTATATTATTCATCCCA 424
QY 301 AGATAATGATGCTGCTTTGACACCTTTGGATCCCAATAAAGAAATATTTTGGGGTCTTAG 360
Db 425 AGATAATGATGCTGCTTTGACACCTTTGGATCCCAATAAAGAAATATTTTGGGGTCTTAG 484
QY 361 CAATTTCTTGGAAACACACTGGCTTTATGGCAACATTTTGGAGTTACTCTTTGGTTCAAT 420

; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 ; STREET: 6300 Sears Tower, 233 South Wacker Drive
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: United States of America
 ; ZIP: 60606-6402
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/729,402
 ; FILING DATE: 04-Dec-2000
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/318,905
 ; FILING DATE: 06-OCT-1994
 ; APPLICATION NUMBER: US 08/133,803
 ; FILING DATE: 06-OCT-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: No. US20010021379Aland, Gretta E.
 ; REGISTRATION NUMBER: 35,302
 ; REFERENCE/DOCKET NUMBER: 27866/32793
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (312) 474-6300
 ; TELEFAX: (312) 474-0448
 ; TELEX: 25-3658
 ; INFORMATION FOR SEQ ID NO: 30:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1335 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 30:
 ; US-09-729-402-30

Query Match 85.4%; Score 1162.4; DB 9; Length 1335;
 Best Local Similarity 92.4%; Pred. No. 1.5e-309;
 Matches 1223; Conservative 0; Mismatches 101; Indels 0; Gaps 0;
 Qy 38 ATGGTGCCACCAAAATGCGATGCTTTCTGCGCTGCGCGCTGCGCTGCGCTGCGCTTAT 97
 Db 1 ATGGTACCCCAAGTCGACGCTCTGTTTGTCTGTGTGATGCTCGCGCTGCTGAC 60
 Qy 98 CCTTTTACCTGGCAATACATAAATCTGTTGCCATATGAATCATCAGCATGGTCAAC 157
 Db 61 CCTTTCGATGGCAGTATATCAACCCGCTGCTCAGATGAAGCAGCGCTGGGTGAAT 120
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 Db 121 AAGATCAGGTGCTCATGGCCGACCAAGCTTGGTCAGACCAAGATTCCTAGAGGCAAC 180
 Qy 218 GGGCTTATTCGGTGTGTGACAGCTTAATGTTGATCACAATAAAGGCGACCTTC 277
 Db 181 GGGCCCTACAGCGTGGGCTGACCGATCTGATGTTGACACCATCAACAAAGGAACCTTT 240
 Qy 278 TTGGTTTATATATATCCATCCAGATAATGATCGCTTGACACCCCTTTGGATCCCAAT 337
 Db 241 CTGAGACTGTACTACCCCGACGACGACCAACGACAGACTGGATCTCTGTGATCCCAAT 300
 Qy 338 AAAGAAATATTTTGGGCTGTAGCAAAATTTCTTGGAAACACACTGGCTTATGGGCAACAT 397
 Db 301 AAAGAAATATTTTGGGCTGTAGCAAAATTTCTTGGAAACACACTGGCTTATGGGCAACAT 360
 Qy 398 TTGAGGTACTCTTTGGTTCATGACAACTCTCGCAAACTGGAATCCCTCTGAGGCT 457
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 Qy 578 GATAGATCTGCATCTGCAACTTACTATTTTCAAGGACCAATCTGCTGAGAAATAGGGGAC 637
 Db 541 GATAGATCTGCATCTGCAACTTACTATTTTCAAGGACCAATCTGCTGAGAAATAGGGGAC 600
 Qy 638 AAGTCTTTGGCTCTACCTTTAGAACCTTGAACCAAGAGGAGGAGACACATATACGAAATGAG 697
 Db 601 AAGTCTTTGGCTCTACCTTTAGAACCTTGAACCAAGAGGAGGAGACACATATACGAAATGAG 660
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 Db 661 CAGGTACGGCAAGAGAGCAAAAGAAATGTTTCCCAAGCTCTCAGTCTGATCTTTCGACATTGAT 720
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 Qy 878 CAGACTCTTAGTGAAGATCAGAGATCAGATGTTGGTATTTCCCTTGGATGATGATGATTTT 937
 Db 841 CAGACTCTTAGTGAAGATCAGAGATCAGATGTTGGTATTTCCCTTGGATGATGATGATTTT 900
 Qy 938 CCACTGGGTGATGAAGTATATTCAGAAATTCCTCAGCCCTCTTTTATTCACACTCTGAA 997
 Db 901 CCACTGGGTGATGAAGTATATTCAGAAATTCCTCAGCCCTCTTTTATTCACACTCTGAA 960
 Qy 998 TATTTCCAATATCTGCTAATATATCAAAAATGAAAAATGCTACTCACCTGATAAAGAA 1057
 Db 961 TATTTCCAATATCTGCTAATATATCAAAAATGAAAAATGCTACTCACCTGATAAAGAA 1020
 Qy 1058 AGAAGATGATTAACAATCAGGGGTTGATCCACAGAAATTTTGTGCTGATCTTCACTTTTGA 1117
 Db 1021 AGAAGATGATTAACAATCAGGGGTTGATCCACAGAAATTTTGTGCTGATCTTCACTTTTGA 1080
 Qy 1118 ACTGGCAAAATATTTGGACACATGCTCAAAATTAAGGGGAGACATAGATTCAAATGACGCT 1177
 Db 1081 ACTGGCAAAATATTTGGACACATGCTCAAAATTAAGGGGAGACATAGATTCAAATGACGCT 1140
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 Qy 1358 AATT 1361
 Db 1321 AATT 1324

RESULT 14
 US-10-003-978A-30
 ; Sequence 30, Application US/10003978A
 ; Publication No. US2003007274/1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cousens, Lawrence S.
 ; Eberhardt, Christine D.
 ; Gray, Patrick W.
 ; Le Trong, Hai
 ; Tjoelker, Larry W.

Wilder, Cheryl L.
 TITLE OF INVENTION: Platelet-Activating Factor
 Acetylhydrolase
 NUMBER OF SEQUENCES: 30
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Marshall, Gerstein & Borun
 STREET: 6300 Sears Tower, 233 South Wacker Drive
 CITY: Chicago
 STATE: Illinois
 COUNTRY: United States of America
 ZIP: 60606-6357
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/003,978A
 FILING DATE: 23-Oct-2001
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 09/729,402
 FILING DATE: 04-DEC-2000
 APPLICATION NUMBER: US 09/577,758
 FILING DATE: 23-MAY-2000
 APPLICATION NUMBER: US 09/010,715
 FILING DATE: 22-JAN-1998
 APPLICATION NUMBER: US 08/480,658
 FILING DATE: 07-JUN-1995
 APPLICATION NUMBER: US 08/318,905
 FILING DATE: 06-OCT-1994
 APPLICATION NUMBER: US 08/133,803
 FILING DATE: 06-OCT-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: No. US2003007274/aland, Greta B.
 REGISTRATION NUMBER: 35,302
 REFERENCE/DOCKET NUMBER: 27866/37792
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (312) 474-6300
 TELEFAX: (312) 474-0448
 INFORMATION FOR SEQ ID NO: 30:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1335 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 SEQUENCE DESCRIPTION: SEQ ID NO: 30:

us-10-003-978A-30
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 Best Local Similarity 92.4%; Pred. No. 1.5e-309;
 Matches 1223; Conservative 0; Mismatches 101; Indels 0; Gaps 0;
 QY 38 ATGGTGCCACCAATTCATGCTTTCTGCTCTGCGGCTCCCTGGCTGCTGTTAT 97
 DB 1 ATGGTACCCCAAGCTGCACGCTCTGTTTGTCTGTGGATGTCGCGCGTGTAC 60
 QY 98 CTTTTCAGTGGCAATACATAATCTGTTGCCCATATGAATCATCAGCATGGTCAAC 157
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 QY 158 AAAATACAACTACTGATGGCTGCTGCAAGCTTTGGCCAAACTAAATCCCCCGGGAAAT 217
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 QY 218 GGGCTTATTCGGTGTGTAGCAGCTTAATGTTGATCACACTAATAAGGCACTTC 277
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 QY 278 TTGGTTTATATATCCATCCAGATATGATGCTTGACACCTTTGGATCCCAAT 337
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QY 338 AAAGATATTTTGGGGTCTTAGCAATTTCTTGGAAACACACACTGGCTTATGGGCAACATT 397
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 QY 458 GGTGAAAAATATCCACTTTGTTGTTTTCTCATGCTTTGGGGCAATTCAGGACACTTTAT 517
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 DB 481 TCTGCTATTGGCAATTCACCTTGGCATCTCATGGGTTTATAGTTGCTGCTGAGAACACAGA 540
 QY 578 GATAGATCTGCACTCTGCAACTTACTATTTCAAGGACCAATCTGCTGAGAAATAGGGGAC 637
 DB 541 GATAGATCTGCACTCTGCAACTTACTATTTCAAGGACCAATCTGCTGAGAAATAGGGGAC 600
 QY 638 AAGTCTTGGCTCTACCTTAGAACCTTGAACCAAGAGAGGAGACACATATACGAATGAG 697
 DB 601 AAGTCTTGGCTCTACCTTAGAACCTTGAACCAAGAGAGGAGACACATATACGAATGAG 660
 QY 698 CAGGTACGGCAAGAGAGCAAAAGAAATGTTCCCAAGCTCTCAGTCTGATTTCTTGACATTGAT 757
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 DB 1261 AACATTAAACAAACCAATCAACACATCATGTTTACGAACCTCTTCAGGAATAGAGAAATAC 1320
 QY 1358 AATT 1361
 DB 1321 AATT 1324


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Db      1349 GCCATTCTGCAGAACTCCACAGGAATAGAGAGACCAATT 1388

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Search completed: March 16, 2005, 06:35:27
Job time : 1328.88 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 15, 2005, 09:15:21 ; Search time 5497.71 Seconds

(without alignments)
9423.093 Million cell updates/sec

Title: US-09-922-067F-9

Perfect score: 1361

Sequence: 1 tgagagactaaagctgaaact.....aggaatagagaatacaatt 1361

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_est3:*

4: gb_est4:*

5: gb_est5:*

6: gb_est6:*

7: gb_est7:*

8: gb_est8:*

9: gb_est9:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1351.4	99.3	1562	3	CR608325	CR608325 full-length
2	1348.4	99.1	1793	3	BC025674	BC025674 Homo sapi
3	1346.4	98.9	1531	3	CR615354	CR615354 full-length
4	1255.2	92.2	1326	9	AY407445	AY407445 Homo sapi
5	1247.7	91.6	1326	9	AY407446	AY407446 Pan trogl
6	920.2	67.6	1022	1	AL575852	AL575852 full-length
7	888.4	65.3	1158	3	CR608291	CR608291 full-length
8	881.1	62.7	946	1	AL573565	AL573565 full-length
9	856.6	62.9	1011	1	AL554852	AL554852 full-length
10	808.2	59.4	1890	3	AK051454	AK051454 Mus muscu
11	785.2	57.7	1695	3	AK005210	AK005210 Mus muscu
12	761.2	55.9	1007	1	AL552617	AL552617 full-length
13	747.6	54.9	935	1	AL549288	AL549288 full-length
14	738.2	54.2	1326	9	AY407447	AY407447 Mus muscu
15	692.4	50.9	734	6	CA312081	CA312081 UI-CF-FNO
16	643.6	47.3	1376	3	AK005158	AK005158 Mus muscu
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18	592.4	43.5	594	7	CK903738	CK903738 ie64e09.Y
19	590.2	43.4	900	4	BG530083	BG530083 602558743
20	583.2	42.9	825	1	BI768378	BI768378 603053686
21	571.2	42.0	650	4	AI343491	AI343491 tb97c04.x
22	566.6	41.6	835	5	BP168449	BP168449 BP168449
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24	552.4	40.6	554	4	BI964070	BI964070 ie64e09.Y

25	550	40.4	584	5	BP296533	BP296533
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27	529.6	38.9	874	4	BI182205	BI182205 UNL-P-FN-
28	529.2	38.9	733	4	BI912346	BI912346 603067687
C 29	513.6	37.7	598	2	BF509203	BF509203 UI-H-B14-
C 30	497.4	36.5	519	2	AW071677	AW071677 w53b01.x
C 31	490.4	36.0	875	4	BI688832	BI688832 603311546
C 32	486.2	35.7	751	5	BP439513	BP439513 BP439513
C 33	483.8	35.5	560	2	BF508812	BF508812 UI-H-B14-
C 34	481.2	35.4	622	4	BM536645	BM536645 ha72f11.g
C 35	475.6	34.9	849	7	CK022811	CK022811 AGENCOURT
C 36	475	34.9	934	5	BU506078	BU506078 AGENCOURT
C 37	474.2	34.8	858	4	BI772693	BI772693 603053447
C 38	472.4	34.7	561	5	BP301477	BP301477 BP301477
C 39	467	34.3	505	5	BQ011547	BQ011547 UI-1-BC1p
C 40	463.2	34.0	679	5	BP459594	BP459594 BP459594
C 41	462.6	34.0	708	5	BP147696	BP147696 BP147696
C 42	461.4	33.9	876	4	BI665978	BI665978 603287028
C 43	454.8	33.4	750	4	BI689361	BI689361 603315803
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C 45	449.2	33.0	995	6	BY705386	BY705386 BY705386

ALIGNMENTS

RESULT 1	CR608325	1562 bp	mRNA	linear	HTC 21-JUL-2004
LOCUS	CR608325	full-length cDNA clone	CSODI067YM18 of Placent	Cot 25-normalized	
DEFINITION	CR608325	of Homo sapiens (human).			
ACCESSION	CR608325	CR608325.1	GI:50489132		
VERSION	CR608325.1	HTC; CDS; CDS			
KEYWORDS	HTC; CDS; CDS				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
REFERENCE	1	(bases 1 to 1562)			
AUTHORS	Li, W.B., Gruber, C., Jessee, J., and Polayes, D.				
TITLE	Full-length cDNA libraries and normalization				
JOURNAL	Unpublished				
REMARK	Contact: Feng Liang Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue				
REFERENCE	2	(bases 1 to 1562)			
AUTHORS	Genoscope.				
TITLE	Direct Submission				
JOURNAL	Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage				

COMMENT
BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr)
- Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of invitrogen.

FEATURES
source
1..1562
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODI067YM18"
/tissue type="Placent
/plasmid="pCMVSPORT_6"

ORIGIN	Query Match	99.3%	Score 1351.4	DB 3	Length 1562
	Best Local Similarity	99.9%	Pred. No. 0		
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				Indels	0
				Gaps	0
OY	1	TGAGAGACTAAGCTGAACTGCTGCTCAGCTCCCAAGATGGTCCCAATTCATCT	60		
DB	210	TGAGAGACTAAGCTGAACTGCTGCTCAGCTCCCAAGATGGTCCCAATTCATCT	269		

Qy	61	GCTTTTCTGCCTCTCGGGCTGCCTGGCTGGTTATCCTTTTGACTGGCAATACATAAA	120
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Db	630	GACAACTCCTGCAAACTGGAAATCCCTCTCTGAGGCCCTGGTGA AAAATATCCACTTGTGT	689
Qy	481	TTTTTCTCATGGTCTTGGGGATTCAGGACACTTATCTGCTATTGGCAATTGACCTGGC	540
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Db	930	ATGTTTCCCAAGCTCTCAGCTGATCTTTGA CATTGATCATGGAAGCCAGTGAAGATGC	989
Qy	781	ATTAGATTTAAGTTTGATATGGAAACAACCTGAAGGACTCTATTGATAGGGA AAAATAGC	840
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Qy	901	ATTCAGATGTGATATGGCCCTGGATGCAATGGATGTTTCCACTGGGTGATGAAGTATATTC	960
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Qy	1021	CATAAAAATGAAAAAATGCTACTCACTCTATAAAGAAAGAAATGATTACAAATCAGGGG	1080
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Qy	1081	TTTCAGTCCACAGAAATTTTGCTGACTTCACTTTTGGCACTGGCAAAAATTAATTGACACAT	1140
Db	1290	TTTCAGTCCACAGAAATTTTGCTGACTTCACTTTTGGCACTGGCAAAAATTAATTGACACAT	1349

Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaapi, R., Maduro, Q. L., Masiello, C., Maskeri, B., Mastrian, S. D., McCloskey, J. C., McDowell, J., Pearson, R., Stantripop, S., Thomas, P. J., Touchman, J. W., Young, A., Vogt, J. L., Walker, M. A., Wetherby, K. D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E. D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAC Plate: 49 Row: e Column: 9
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 31543409
This clone has the following problem: frame shifted.

FEATURES

Location/Qualifiers

source

1..1793
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5203018"
/tissue_type="Lung, Spleen, fetal, pooled"
/clone_lib="NIH MGC_122"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"

ORIGIN

Query Match 99.1%; Score 1348.4; DB 3; Length 1793;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1360; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 TGAGAGACTAAGCTGAACTGCTGCTCAGCTCCCAAGATGGTGCACCCCAAAATTCGATGT 60
DB 161 TGAGAGACTAAGCTGAACTGCTGCTCAGCTCCCAAGATGGTGCACCCCAAAATTCGATGT 220
QY 61 GCTTTTCTGCTCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
DB 221 GCTTTTCTGCTCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 280
QY 121 TCCTGTTGCCCATGATGAATCATCAGCATGGTGCACCAAAATACAGTACTGATGCTGCTC 180
DB 281 TCCTGTTGCCCATGATGAATCATCAGCATGGTGCACCAAAATACAGTACTGATGCTGCTC 340
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DB 461 AGATAATGATCGCTTGACACCTTTGGATCCCAATTAAGATATTTTGGGGTCTTAG 520
QY 361 CAAATTTCTGGAAACACACTGGCTTATGGGCAACATTTTGGAGGTACTCTTTGGTTCAAT 420
DB 521 CAAATTTCTGGAAACACACTGGCTTATGGGCAACATTTTGGAGGTACTCTTTGGTTCAAT 580
QY 421 GACAACTCTGCAAACTGGAATTCCTCTGTAGGCGCTGGTGAATAATATCCACTTGTGT 480
DB 581 GACAACTCTGCAAACTGGAATTCCTCTGTAGGCGCTGGTGAATAATATCCACTTGTGT 640
QY 481 TTTTCTCATGCTTGGGCACTTGGGCACTTGGGCACTTGGGCACTTGGGCACTTGGGCACTTGGG 540
DB 641 TTTTCTCATGCTTGGGCACTTGGGCACTTGGGCACTTGGGCACTTGGGCACTTGGGCACTTGGG 700
QY 541 ATCTCATGGTTTATAGTCTGCTGTAGAACACAGATAGATCGCATCTGCAACTTA 600
DB 701 ATCTCATGGTTTATAGTCTGCTGTAGAACACAGATAGATCGCATCTGCAACTTA 760
QY 601 CTATTTCAAGGACCAATCTGCTGCAGAAATAGGGGCAAGTCTTGGCTCTTACCTTAGAAC 660
DB 761 CTATTTCAAGGACCAATCTGCTGCAGAAATAGGGGCAAGTCTTGGCTCTTACCTTAGAAC 820
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DB 881 ATGTTTCCCAGAGCTCTCAGTCTGATTTCTTGACATTTGATCATGGAAAGCCAGTGAAGATGC 940
QY 781 ATTAGATTTAAAGTTTGATATGGAACAACTGAAGGACTCTATTGTAGTGGGAAAAATATAGC 840
DB 941 ATTAGATTTAAAGTTTGATATGGAACAACTGAAGGACTCTATTGTAGTGGGAAAAATATAGC 1000
QY 841 AGTAAATTGACATTTCTTTTGGTGGAGCAACGGTTATTTCAGACTCTTAGTCAAGATCAGAG 900
DB 1001 AGTAAATTGACATTTCTTTTGGTGGAGCAACGGTTATTTCAGACTCTTAGTCAAGATCAGAG 1060
QY 901 ATTACAGATGTGTTATTTGCCCTGGATGCATGGATGTTTCCACTGGGTGATGAAGTATATTC 960
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QY 961 CAGAAATCTCAGCCCTCCTCTTTTATCAACTCTGAAATATTTCCAAATATCTCTGCTAATA 1019
DB 1121 CAGAAATCTCAGCCCTCCTCTTTTATCAACTCTGAAATATTTCCAAATATCTCTGCTAATA 1180
QY 1020 TCATAAAATGAAATAATGCTACTCACCTGATAAAGAAAGAGAGATGATTACAAATCAGGG 1079
DB 1181 TCATAAAATGAAATAATGCTACTCACCTGATAAAGAAAGAGATGATTACAAATCAGGG 1240
QY 1080 GTTCAGTCCACCAGAAATTTTGTGCTGCTTTCACCTTTTGCACCTGGCAAAATAATTTGGACACA 1139
DB 1241 GTTCAGTCCACCAGAAATTTTGTGCTGCTTTCACCTTTGCACTGGCAAAATAATTTGGACACA 1300
QY 1140 TGTCTAAATTAAGGGAGACATAGATTCAAATGACAGTATTGATCTTAGCAACAAAGCTT 1199
DB 1301 TGTCTAAATTAAGGGAGACATAGATTCAAATGACAGTATTGATCTTAGCAACAAAGCTT 1360
QY 1200 CATTAGCATCTTACAAAGAGCTTTAGGACTTTCATTAAGATTTTGTAGTGGGACTGCT 1259
DB 1361 CATTAGCATCTTACAAAGAGCTTTAGGACTTTCATTAAGATTTTGTAGTGGGACTGCT 1420
QY 1260 TGATTTGAAGGAGATGATGAGAACTTTATTTCCAGGGACCAACATTAACAAACCAATCAAC 1319
DB 1421 TGATTTGAAGGAGATGATGAGAACTTTATTTCCAGGGACCAACATTAACAAACCAATCAAC 1480
QY 1320 ACATCATGTTACAGAACTCTTCAGGAATAGAGAAATACAATT 1361
DB 1481 ACATCATGTTACAGAACTCTTCAGGAATAGAGAAATACAATT 1522

RESULT 3

CR615354

LOCUS

DEFINITION

full-length cDNA clone CS0DI049VE02 of Placenta Cot 25-normalized

of Homo sapiens (human).

ACCESSION

CR615354

VERSION

CR615354.1 GI:50496161

KEYWORDS

HTC; CNSLT_cDNA.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

AUTHORS

Li, W.B., Gruber, C., Jesse, J. and Polayes, D.

TITLE

Full-length cDNA libraries and normalization

JOURNAL

Unpublished

REMARK

Contact : Feng Liang Email : liang@lifetech.com URL : <http://fulllength.invitrogen.com/> Invitrogen Corporation 1600 Faraday Avenue 2 (bases 1 to 1531)

REFERENCE

AUTHORS

Genoscope.

TITLE

Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

[illegible]

QY 469 TCACCTGTTGTTTCTTCATGCTCTGGGCAATTCAGGACACTTTATTTCTGCTATTGG 528
Db 885 TCACCTGTTGTTTCTTCATGCTCTGGGCAATTCAGGACACTTTATTTCTGCTATTGG 826
QY 529 CATTGACCTGGCACTCTCATGGGTTTATAGTTGCTGTGTAGAAACACAGAGATAGATCTGC 588
Db 825 CATTGCCCTGGCACTCTCATGGGTTTATAGTTGCTGTGTAGAAACACAGAGATAGATCTGC 766
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QY 709 AAGAGCAAAAGAAATGTTCCCAAGCTCTCAGTCTGATTTCTTGACATTCATGATGAAAGCC 768
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QY 769 AGTGAAGAAATGCAATGATTTAAAGTTGATATGGAACAACTGAAGGACTCTATTGATAG 828
Db 585 AGTGAAGAAATGCAATGATTTAAAGTTGATATGGAACAACTGAAGGACTCTATTGATAG 526
QY 829 GGAAGAAATAGCAGTAAATCGACATCTCTTTGTTGGAGCAACGGTTATTCAGACTCTTAG 888
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QY 1009 TCCTGCTAATATCATAAAATGAATGCTACTACCTGATATGAAAGAAAGATGAT 1068
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QY 1069 TACAATCAGGGGTTTCACTCACCAGAAATTTTGCTGACTTCACTTTTGCACTGGCAAAAT 1128
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QY 1189 CAACAAGCTTCAATAGCACTTCTTACAAAGCAATTTAGGACTTCAATTAAGATTTGATCA 1248
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QY 1249 GTGGGACTGCTGATTGAAGGAGATGATAGAAATCTTATTCAGGGACCAACATTAACAC 1308
Db 105 GTGGGACTGCTGATTGAAGGAGATGATAGAAATCTTATTCAGGGACCAACATTAACAC 46
QY 1309 AACCAATCAACATCATGTTACAGAACTCTTCAGGAATAGAA 1353
Db 45 AACCAATCAACATCATGTTACAGAACTCTTCAGGAATAGAA 1

RESULT 7
LOCUS CR608291
DEFINITION full-length cDNA clone CS0D1087Y019 of Placenta Cot 25-normalized of Homo sapiens (human).
ACCESSION CR608291
VERSION CR608291.1 GI:50489098
KEYWORDS HTC; CDS; cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Euthera; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 1158)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paradise Avenue
2 (bases 1 to 1158)
Genoscope.
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
ends enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
Location/Qualifiers
source
1..1158
/organism="Homo sapiens"
/mol type="mRNA"
/db xref="taxon:9606"
/clone="CS0D1087Y019"
/tissue type="Placenta Cot 25-normalized"
/plasmid="pCMVSPORT_6"
ORIGIN
Query Match 65.3%; Score 888.4; DB 3; Length 1158;
Best Local Similarity 99.9%; Pred. No. 4.1e-232;
Matches 889; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 TGAGAGACTAAGCTGAACTGCTGCTCAGCTCCCAAGATGGTCCCAACCAATTCGATGT 60
Db 124 TGAGAGACTAAGCTGAACTGCTGCTCAGCTCCCAAGATGGTCCCAACCAATTCGATGT 183
QY 61 GCTTTTCTGCTCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
Db 184 GCTTTTCTGCTCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 243
QY 121 TCTGTTGGCCCATATCAAAATCATCAGCATGGGTCAACAAATACAAATACAAATACAAAT 180
Db 244 TCTGTTGGCCCATATCAAAATCATCAGCATGGGTCAACAAATACAAATACAAATACAAAT 303
QY 181 TGCAAGCTTTGGCCAACTAAATCCCGGGGAAATGGGCTTATTCCTGTTGGTGTAC 240
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QY 241 AGACTTAATGTTTGATCACAATAAAGGACCTTCTTGGCGTTTATATATATCCATCCCA 300
Db 364 AGACTTAATGTTTGATCACAATAAAGGACCTTCTTGGCGTTTATATATATCCATCCCA 423
QY 301 AGATAATGATCGCTTGCACACCTTTGGATCCCAATTAAGATATTTTGGGGTCTTAG 360
Db 424 AGATAATGATCGCTTGCACACCTTTGGATCCCAATTAAGATATTTTGGGGTCTTAG 483
QY 361 CAAATTTCTGGAAACACACTGGCTTATGGGCAACATTTTGGAGTTACTCTTTGGTCAAT 420
Db 484 CAAATTTCTGGAAACACACTGGCTTATGGGCAACATTTTGGAGTTACTCTTTGGTCAAT 543
QY 421 GACAACTCTGCAAACTGGAAATTCCTCTCTGAGGCTGTGGGAAATATATCCACTTGTGT 480
Db 544 GACAACTCTGCAAACTGGAAATTCCTCTCTGAGGCTGTGGGAAATATATCCACTTGTGT 603
QY 481 TTTTCTCATGCTCTTGGGGCAATTCAGACACTTTATTTCTGCTATTTGGGCACTGCTGCG 540
Db 604 TTTTCTCATGCTCTTGGGGCAATTCAGACACTTTATTTCTGCTATTTGGGCACTGCTGCG 663
QY 541 ATCTCATGGGTTTATAGTTGCTGCTAGAAACACAGAGATAGATCTGCACTCTGCACTTA 600
Db 664 ATCTCATGGGTTTATAGTTGCTGCTAGAAACACAGAGATAGATCTGCACTCTGCACTTA 723

AUTHORS TITLE JOURNAL COMMENT

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 15, 2001 this sequence version replaced gi:31276662.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, Cp 5706 - 91057 EVRY cedex - FRANCE
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
3382.r

For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?c=CSODI087AH10QPI&c=3382.r.

FEATURES

source

Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODI087Y019"
/cissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 62.9%; Score 856.6; DB 1; Length 1011;
Best Local Similarity 98.4%; Pred. No. 2,1e-223;
Matches 871; Conservative 4; Mismatches 8; Indels 2; Gaps 1;
QY 1 TGAGAGCTAAGCTGAAGTCTGCTCAGCTCCCAAGATGGTCCACCAATTCATGT 60
DB 124 TGAGAGCTAAGCTGAAGTCTGCTCAGCTCCCAAGATGGTCCACCAATTCATGT 183
QY 61 GCTTTTCGCTCTCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
DB 184 GCTTTTCGCTCTCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 243
QY 121 TCCTGTTCCCATATGAATCATCAGCATGGTCAACAAATACAAATACAGTCTGCTGC 180
DB 244 TCCTGTTCCCATATGAATCATCAGCATGGTCAACAAATACAAATACAGTCTGCTGC 303
QY 181 TGCAAGCTTTGGCCAACTAAATCCCGGGGAAATGGGCTTATTCGGTTGGTTGTAC 240
DB 304 TGCAAGCTTTGGCCAACTAAATCCCGGGGAAATGGGCTTATTCGGTTGGTTGTAC 363
QY 241 AGACTTAATGTTGATCATCACTAATAAGGCACTCTTGGTGTATATATCAATCCCA 300
DB 364 AGACTTAATGTTGATCATCACTAATAAGGCACTCTTGGTGTATATATCAATCCCA 423
QY 301 AGATAATGATCGCTTGACACCTTTGGATCCCAATAAAGATATTTTGGGGTCTTAG 360
DB 424 AGATAATGATCGCTTGACACCTTTGGATCCCAATAAAGATATTTTGGGGTCTTAG 483
QY 361 CAAATTTCTTGGAAACACACTGGCTTATGGGCAACATTTTGGGTTACTCTTTGGTTCAAT 420
DB 484 CAAATTTCTTGGAAACACACTGGCTTATGGGCAACATTTTGGGTTACTCTTTGGTTCAAT 543
QY 421 GACAACTCCTGAACTGGAAATTCCTCTGAGGCTGGTGAATAATTCACATTTGTT 480
DB 544 GACAACTCCTGAACTGGAAATTCCTCTGAGGCTGGTGAATAATTCACATTTGTT 603
QY 481 TTTTTCATGCTCTTGGGGCAATCAGGACATTTATTCGCTATTCGCTATTCGCTGGC 540
DB 604 TTTTTCATGCTCTTGGGGCAATCAGGACATTTATTCGCTATTCGCTATTCGCTGGC 663
QY 541 ATCTCATGGGTTTATGTTGCTGCTGTAGAACACAGAGATAGATCTGCATCTGCAACTTA 600
DB 664 ATCTCATGGGTTTATGTTGCTGCTGTAGAACACAGAGATAGATCTGCATCTGCAACTTA 723

QY 601 CTATTTCAAGGACCAATCTGCTGCGAATATAGGGGCAAGTCTTGCTCTTACTTAGAAC 660
DB 724 CTATTTCAAGGACCAATCTGCTGCGAATATAGGGGCAAGTCTTGCTCTTACTTAGAAC 783
QY 661 CTTGAAACACAGAGGAGGAGACACATATACGAATACGACAGGTACGCAAGAGCAACAGA 720
DB 784 CTTGAAACACAGAGGAGGAGACACATATACGAATACGACAGGTACGCAAGAGCAACAGA 843
QY 721 ATGTTCCCAAGCTCTCAGTCTGATTTTTCGACATTCATGGAAGCCAGTGAAGAATGC 780
DB 844 ATGTTCCCAAGCTCTCAGTCTGATTTTTCGACATTCATGGAAGCCAGTGAAGAATGC 903
QY 781 ATTAGATTAAAGTTTATGATATGGAACAACTGAAGACTCTTATGATAGGAAAAAATAGC 840
DB 904 ATTAGATTAAAGTTTATGATATGGAACAACTGAAGACTCTTATGATAGGAAAAAATAGC 963
QY 841 AGTAATTCGACATCTTTTGGTGGAGCAACGCTTATTCAGACTCT 885
DB 964 AGTAATTCGACATCTTTTGGGTTG--YGCAMSGKTAATCAGACTCT 1006

RESULT 10
AK051454

LOCUS
DEFINITION

AK051454 1890 bp mRNA linear HTC 03-APR-2004
Mus musculus 12 days embryo spinal ganglion cDNA, RIKEN full-length
enriched library, clone:DJ3049018 product:phospholipase A2 group
VII (platelet-activating factor acetylhydrolase, plasma), full
insert sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

AK051454.1 GI:26341969
HTC; CAP trapper.
Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

High-efficiency full-length cDNA cloning
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Kashiwagi, K.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium

TITLE

JOURNAL

MEDLINE

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REFERENCE

JOURNAL REFERENCE AUTHORS	Nature 420, 563-573 (2002)	Db
6 (bases 1 to 1890)	Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayaehida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, P., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, K., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.	459
TITLE JOURNAL	Direct Submission Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gs.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)	185
COMMENT	cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL: http://genome.gsc.riken.jp/ URL: http://fantom.gsc.riken.jp/ Location/Qualifiers	516
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CDS	Query Match 59.4%; Score 808.2; DB 3; Length 1890; Best Local Similarity 75.2%; Pred. No. 4.7e-210; Matches 1021; Conservative 0; Mismatches 333; Indels 3; Gaps 1; 5 AGACTAAGCTGAACCTGCTGCTCAGCTCCCAAGATGGTCCACCCAAATATGCATGCTT 64 339 ACATCAAACTGAAGCCACCTGCTCAGCTCCCTAAGATGGTACCACCTCAAACCTGACGCGCTT 398 65 TTCTGCTCTCGCGCTCCCTCGCTGGTGTGTTATCTCTTTTGACTGGCAATACATAAATCCT 124 399 TTCTGCTCTCTGCTGCTCCCATGGTCCATCTCTTTTCACTGGCAAGACACATCTTCT 458 125 GTTCCCATATGAATCATCAGCATGGGTCAACAAATACAGTACTGATGCTGCTGCA 184	1024
ORIGIN	Query Match 59.4%; Score 808.2; DB 3; Length 1890; Best Local Similarity 75.2%; Pred. No. 4.7e-210; Matches 1021; Conservative 0; Mismatches 333; Indels 3; Gaps 1; 5 AGACTAAGCTGAACCTGCTGCTCAGCTCCCAAGATGGTCCACCCAAATATGCATGCTT 64 339 ACATCAAACTGAAGCCACCTGCTCAGCTCCCTAAGATGGTACCACCTCAAACCTGACGCGCTT 398 65 TTCTGCTCTCGCGCTCCCTCGCTGGTGTGTTATCTCTTTTGACTGGCAATACATAAATCCT 124 399 TTCTGCTCTCTGCTGCTCCCATGGTCCATCTCTTTTCACTGGCAAGACACATCTTCT 458 125 GTTCCCATATGAATCATCAGCATGGGTCAACAAATACAGTACTGATGCTGCTGCA 184	1084

Db 1536 GCTTTCTTACAAAGCACTTTAGGCGCTTCAGAAAGCACTTGTGATCAGTGGGACCCCTCTCGTG 1595

Qy 1265 GAAGGAGATGATGAGATCTTTATTTCCAGGGACCAACATTAACACAAACCAATCAACACATC 1324

Db 1596 GAAGGAGATGATGAGAACCTGATTTCTTGGGTACCCCTTTGAGCGCAGTCACCCAGGTCCCG 1655

Qy 1325 ATGTTACAGAACCTTTCCAGGATAGAGAAATACAAATT 1361

Db 1656 GCTCAGCAACACCTCTCCAGGATCACAGACCCAGAATT 1692

RESULT 11

AK005210

LOCUS

DEFINITION Mus musculus adult male cerebellum cDNA, RIKEN full-length enriched library, clone:1500011H20 product:phospholipase A2 group VII (platelet-activating factor acetylhydrolase, plasma), full insert sequence

ACCESSION AK005210

VERSION AK005210.1 GI:12837612

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS Carninci,P. and Hayashizaki,Y.

TITLE High-efficiency full-length cDNA cloning

JOURNAL Meth. Enzymol. 303, 19-44 (1999)

MEDLINE 93279253

PubMed 10349636

REFERENCE 2

AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL Genome Res. 10 (10), 1617-1630 (2000)

MEDLINE 20499374

PubMed 11042159

REFERENCE 3

AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kiteunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwaki,S., Inoue,K., Togawa,Y., Izawa,M., Ohata,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.

TITLE RIKEN integrated sequence analysis (RISA) system--384-Format sequencing pipeline with 384 multicapillary sequencer

JOURNAL Genome Res. 10 (11), 1757-1771 (2000)

MEDLINE 20530913

PubMed 11076861

REFERENCE 4

AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.

TITLE Functional annotation of a full-length mouse cDNA collection

JOURNAL Nature 409, 685-690 (2001)

REFERENCE 5

AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)

REFERENCE 6

AUTHORS Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Arai,A., Aono,H., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Fukunishi,Y., Hirano,M., Hanagaki,T., Hara,A., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kasukawa,T., Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C., Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y.,

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RESULT 12
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 DEFINITION
 clone CS0D1067YM18 5-PRIME, mRNA sequence.

AL552617
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 Homo sapiens (human)
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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 1007)
 Li.W.B., Gruber,C., Jessee,J. and Polayes,D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 On Feb 15, 2001 this sequence version replaced gi:31274432.
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 2 rue Gaston Crémieux, CP 5706 - 91057 EVRY cedex - FRANCE
 Email: segre@genoscope.cns.fr, Web : www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
 was normalized. Library was constructed by Life Technologies, a
 division of Invitrogen. This sequence belongs to sequence cluster
 3382.r
 For more information about this cluster, see
 http://www.genoscope.cns.fr/cdna?s=CS0D1067BG090P1&c=3382.r.
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 /note="1st strand cDNA was primed with a NotI-oligo (dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
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 Best Local Similarity 98.6%; Pred. No. 3.1e-197;
 Matches 785; Conservative 3; Mismatches 6; Indels 2; Gaps 2;
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 629 GACAACTCTCGAACTGGAAATTCCTCTGAGGCTGGTGAATAATATCCACTTTGTGT 688

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT
 FEATURES
 source

Thu Mar 17 08:25:04 2005

14671302	PUBMED	2 (bases 1 to 1326)	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferrera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
14671302	REFERENCE	2 (bases 1 to 1326)	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferrera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
14671302	AUTHORS	2 (bases 1 to 1326)	Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferrera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
14671302	TITLE	Direct Submission	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
14671302	JOURNAL	Rockville, MD 20850, USA	This sequence was made by sequencing genomic exons and ordering them based on alignment.
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14671302		Best Local Similarity 70.4%; Pred. No. 6.8e-191;	
14671302		Matches 932; Conservative 0; Mismatches 392; Indels 0; Gaps 0;	
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14671302	Qy	158 AAAATACAGTACTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	217
14671302	Db	121 AAGCTCCAATCGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	180
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14671302	REFERENCE	1 (bases 1 to 734)	
14671302	AUTHORS	Bonaldo,M.F., Lennon,G. and Soares,M.B.	
14671302	TITLE	Normalization and subtraction: two approaches to facilitate gene	
14671302	JOURNAL	Genome Res. 6 (9), 791-806 (1996)	
14671302	MEDLINE	97044477	
14671302	PUBMED	8889548	
14671302	COMMENT	Contact: McCray, PB	
14671302		McCray Lab	
14671302		University of Iowa	
14671302		2024 University of Iowa Med Labs, Iowa City, IA 52242, USA	
14671302		Tel: 319 356 4866	
14671302		Fax: 319 356 7171	
14671302		Email: paul-mccray@uiowa.edu	
14671302		Tissue Procurement: Dr. M. J. Welsh, University of Iowa	
14671302		CDNA Library preparation: Dr. M. Bento Soares, University of Iowa	

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com) or from Open Biosystems (www.openbiosystems.com).
The following repetitive elements were found in this cDNA sequence: 1-24, >At rich#Low_complexity (matched complement)
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES
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/clone="UI-CF-FNO-afj-b-19-0-UI"
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/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-CF-FNO"
/notes="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; UI-CF-FNO is a subtracted cDNA library derived from two normalized human lung epithelial cell libraries (BN1 and DUI). The library was subtracted according to according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. For additional information, contact: bento-soares@uiowa.edu
TAG_TISSUE=Lung Epithelial Cells Tissue nos 359-368
TAG_LIB=UI-CF-FNO
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ORIGIN

Query Match 50.9%; Score 692.4; DB 6; Length 734;
Best Local Similarity 99.6%; Pred. No. 2.1e-178;
Matches 693; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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6	514	100.0	1361 6 AR205614 Sequence
7	514	100.0	1361 6 AX006795 Sequence
8	514	100.0	1505 6 CQ717247 Sequence
9	514	100.0	1554 9 BC038452 Sequence
10	514	100.0	1561 6 AX335487 Sequence
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16	512.4	99.7	1335 6 AR142524 Sequence
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ALIGNMENTS

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LOCUS A41956 1361 bp DNA linear PAT 05-MAR-1997
DEFINITION Sequence 9 from Patent WO9500649.
ACCESSION A41956
VERSION A41956.1 GI:2297493
KEYWORDS .
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 1361)
AUTHORS Macphree,C.H., Tew,D.G., Southan,C.D., Hickey,D.M., Gloger,I.S., Lawrence,G.M. and Rice,S.Q.
TITLE LIPOPROTEIN ASSOCIATED PHOSPHOLIPASE A 2?, INHIBITORS THEREOF AND USE OF THE SAME IN DIAGNOSIS AND THERAPY
JOURNAL Patent: WO 9500649-A 9 05-JAN-1995;
SMITHKLINE BEECHAM PLC (GB)
COMMENT Other publication JP 8500740T 960130.
FEATURES
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Best Local Similarity 100.0%; Pred. No. 1.6e-106; Indels 0; Gaps 0;
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LOCUS ARI125358 1361 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 9 from patent US 6177257.
ACCESSION ARI125358
VERSION ARI125358.1 GI:14111420
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1361)
AUTHORS Macphree, C. Houston., Tew, D. Graham., Southan, C. Donald., Hickey, D. Mary. Bernadette., Gloger, I. Simon., Lawrence, G. Mark. Prouse. and Rice, S. Quentyn John.
TITLE Lipoprotein associated phospholipase A2, inhibitors thereof and use of the same in diagnosis and therapy
JOURNAL Patent: US 6177257-A 9 23-JAN-2001;
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LOCUS BD242703 1361 bp DNA linear PAT 17-JUL-2003
DEFINITION Method for purifying low-density lipoprotein-associated phospholipase A2 using immobilized metal affinity chromatography.
ACCESSION BD242703
VERSION BD242703.1 GI:33052473
KEYWORDS JP 2002528084-A/1.
SOURCE Homo sapiens (human).
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1361)
AUTHORS Boyd, H. and Tew, D. G.
TITLE Method for purifying low-density lipoprotein-associated phospholipase A2 using immobilized metal affinity chromatography
JOURNAL Patent: JP 2002528084-A 1 03-SEP-2002;
COMMENT SMITHKLINE BEECHAM PLC
OS Homo sapiens (human)
PN JP 2002528084-A/1
PD 03-SEP-2002
PF 27-OCT-1999 JP 2000578462
PR 28-OCT-1998 GB 9823647.4, 28-OCT-1998 GB 9823648.2 PI
HELEN BOYD, DAVID GRAHAM TEW
PC C12N15/09, A61P29/00, C07K1/22, C12N5/10, C12N9/16//A61K38/46, PC C12N15/00,
PC C12N5/00, A61K37/54
CC Method for purifying low-density lipoprotein-associated CC
phospholipase A2
CC using immobilized metal affinity chromatography FH Key
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DEFINITION Sequence 9 from patent US 6369045.
ACCESSION AR205614
VERSION AR205614.1 GI:21503242
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1361)
AUTHORS Macphree,C.Houston., Tew,D.Graham, and Hickey,D.Mary.Bernadette.
TITLE Phospholipase A2 inhibitors thereof and use of same in diagnosis and therapy
JOURNAL Patent: US 6369045-A 9 09-APR-2002;
FEATURES Location/Qualifiers
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LOCUS AX006795 1361 bp DNA linear PAT 06-SEP-2000
DEFINITION Sequence 9 from Patent EP0974663.
ACCESSION AX006795
VERSION AX006795.1 GI:9994827
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Gloger,I.S., Hickey,D.M., Macphree,C.H., Southan,C.D., Lawrence,G.M., Rice,S.O. and Tew,D.G.
TITLE Lipoprotein associated phospholipase a2, inhibitors thereof and use of same in diagnosis and therapy
JOURNAL Patent: EP 0974663-A 9 26-JAN-2000;
FEATURES Location/Qualifiers
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RESULT 8
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DEFINITION Sequence 3181 from Patent WO02068579.

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ACCESSION      CQ717247
VERSION        CQ717247.1  GI:42278104
KEYWORDS
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
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               Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS        Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
TITLE          Kits, such as nucleic acid arrays, comprising a majority of
               humanexons or transcripts, for detecting expression and other uses
               thereof
JOURNAL        Patent: WO 02069579-A 3181 06-SEP-2002;
               PE Corporation (NY) (US)
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RESULT 9
LOCUS         BC038452
DEFINITION    Homo sapiens phospholipase A2, group VII (platelet-activating
               factor acetylhydrolase, plasma), mRNA (cdna clone MGC:46165
               IMAGE:5216829), complete cds.
ACCESSION     BC038452
VERSION       BC038452.1  GI:23512330
KEYWORDS      MGC.
SOURCE        Homo sapiens (human)
ORGANISM      Homo sapiens

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Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1554)
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenman, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Datchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Spapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
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Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, R.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
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Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalios, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
12477932
2 (bases 1 to 1554)
Strausberg, R.
Direct Submission
Submitted (04-OCT-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cagbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov
Akhter, N., Ayale, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Hachighi, P.,
Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,
Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,
McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,
Teurgeson, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
Young, A., Zhang, L.-H. and Green, E.D.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/ILNL at: http://image.llnl.gov
Series: IRAC Plate: 78 Row: 9 Column: 17
This clone was selected for full length sequencing because it
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acetylhydrolase, plasma/intracellular isoform II.
Platelet-activating factor acetylhydrolase (PAP-AH) is a
subfamily of phospholipases A2, responsible for
inactivation of platelet-activating factor through
cleavage of an acetyl group. Three known PAP-AHs are the
brain heterotrimeric PAP-AH I, whose catalytic beta and
gamma subunits are aligned in pfam02266, the
extracellular, plasma PAP-AH (pPAP-AH), and the
intracellular PAP-AH isoform II (PAP-AH II). This family
aligns pPAP-AH and PAP-AH II, whose similarity was
previously noted"
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Best Local Similarity 100.0%; Pred. No. 1.6e-106; Indels 0; Gaps 0;
Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 10
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Sequence 5996 from Patent WO0194629.
ACCESSION AX335487
VERSION AX335487.1 GI:18126206
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Young, P. E., Augustus, M., Carter, K. C., Ebner, R., Endress, G.,
Horrigan, S., Soppet, D. R. and Weaver, Z.
TITLE Cancer gene determination and therapeutic screening using signature
gene sets
JOURNAL Patent: WO 0194629-A 5996 13-DEC-2001;
Avallon Pharmaceuticals (US)
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Best Local Similarity 100.0%; Pred. No. 1.6e-106; Indels 0; Gaps 0;
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LOCUS Human LDL-phospholipase A2 mRNA, complete cds.
DEFINITION
ACCESSION U24577
VERSION U24577.1 GI:1314245
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LOCUS AR064425 1335 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 30 from patent US 5847088.
ACCESSION AR064425
VERSION AR064425.1 GI:5993733
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1335)
AUTHORS Cousens,L.S., Eberhardt,C.D., Gray,P., Trong,H.Le., Tjoelker,L.W.
and Wilder,C.L.
TITLE Antibodies specific for platelet-activating factor acetylhydrolase
JOURNAL Patent: US 5847088-A 30 08-DEC-1998;
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Best Local Similarity 99.8%; Pred. No. 3.8e-106;
Matches 513; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DEFINITION Sequence 30 from patent US 5977308.
ACCESSION AR083776
VERSION AR083776.1 GI:10010547
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1335)
AUTHORS Cousens,L.S., Eberhardt,C.D., Gray,P., Trong,H.Le., Tjoelker,L.W.
and Wilder,C.L.
TITLE Platelet-activating factor acetylhydrolase
JOURNAL Patent: US 5977308-A 30 02-NOV-1999;
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Matches 513; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DEFINITION Sequence 30 from patent US 6146625.
ACCESSION AR141171
VERSION AR141171.1 GI:15100688
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1335)
AUTHORS Cousens,L.S., Eberhardt,C.D., Gray,P., Trong,H.Le., Tjoelker,L.W.

and Wilder, C.L.

TITLE Platelet-activating factor acetylhydrolase

JOURNAL Patent: US 6148625-A 30 14-NOV-2000;

FEATURES Location/Qualifiers

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

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Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: Geneseq2001as.*
5: Geneseq2001bs.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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5	512.4	99.7	1203	10	ADG73659 Human PAF
6	512.4	99.7	1335	2	AAT87072 Human pla
7	512.4	99.7	1335	3	AAA10885
8	512.4	99.7	1335	3	AAZ24261 Human PAF
9	512.4	99.7	1335	4	AAD04165 Human pla
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11	512.4	99.7	1335	5	AAD24740 Human pla
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16	512.4	99.7	1505	12	ADH43822 Human pla
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ALIGNMENTS

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ID AAQ81780 standard; CDNA; 1361 BP.
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AC AAQ81780;
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DT 25-MAR-2003 (revised)
DT 18-AUG-1995 (first entry)
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DE Human T-cell lymphoma lipoprotein-associated phospholipase-A2.
XX
KW T-cell; T-lymphocyte; lipoprotein-associated phospholipase-A2; enzyme;
KW atherosclerosis; diagnosis; therapy; antiarteriosclerotic; sg.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
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PN WO9500649-A1.
XX
PD 05-JAN-1995.
XX
PF 24-JUN-1994; 94WO-GB001374.
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PR 25-JUN-1993; 93GB-00013144.
PR 11-JAN-1994; 94GB-00000413.
XX
PA (SMIK) SMITHLINE BEECHAM PLC.
XX
PI Macphee CH, Tew DG, Southan CD, Hickey DMB, Gloger IS;
PI Lawrence GMP, Rice SQ;
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DR WPI; 1995-052086/07.
DR P-PSDB; AAR64928.
XX
PT Purified lipoprotein associated phospholipase A2 - used to develop prods.
PT for diagnosis and therapy, partic. inhibitors for treatment of
PT atherosclerosis.
XX
PS Claim 8; Page 19; 29pp; English.
XX

CC This sequence encodes an enzyme which may be used in a method of
 CC screening compounds to identify those compounds which inhibit lp-PLA2
 CC which involves contacting isolated lp-PLA2 with a test compound and
 CC measuring the rate of turnover of an enzyme substrate as compared with
 CC the rate of turnover in the absence of the test compound. (Updated on 25-
 CC MAR-2003 to correct PN field.)
 XX
 SQ Sequence 1361 BP; 417 A; 273 C; 278 G; 393 T; 0 U; 0 Other;
 Query Match 100.0%; Score 514; DB 2; Length 1361;
 Best Local Similarity 100.0%; Pred. No. 2.5e-129;
 Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 Db 908 TGTGGTATTCGCCCTGGATGCATGATGTTTCCACTGGGTGATGAAGTATATTCAGAAATT 967
 QY 121 CCTCAGCCCTCTTTTTCATCAACTCTGAATATTTCCAAATATCTGCTAATATCATATAAA 180
 Db 968 CCTCAGCCCTCTTTTTCATCAACTCTGAATATTTCCAAATATCTGCTAATATCATATAAA 1027
 QY 181 ATGAAAAATGCTACTCACCTGATPAAAGAAAGAGATGATTACAATCAGGGGTTTCAGTC 240
 Db 1028 ATGAAAAATGCTACTCACCTGATPAAAGAAAGAGATGATTACAATCAGGGGTTTCAGTC 1087
 QY 241 CACCGAATTTTGGTGCATCTTTCACCTTTGGCACTGGGCAAAATATTCGACATGCTCAAA 300
 Db 1088 CACCGAATTTTGGTGCATCTTTCACCTTTGGCACTGGGCAAAATATTCGACATGCTCAAA 1147
 QY 301 TTAAGGAGACATAGATTCAATGACAGTATTGATCTTAGCAACAAGCTTCATTAGCA 360
 Db 1148 TTAAGGAGACATAGATTCAATGACAGTATTGATCTTAGCAACAAGCTTCATTAGCA 1207
 QY 361 TTCTTACAAAAGCATTTAGGACTTCATAAAGATTTTCATCAGTGGGACTGCTGATTGAA 420
 Db 1208 TTCTTACAAAAGCATTTAGGACTTCATAAAGATTTTCATCAGTGGGACTGCTGATTGAA 1267
 QY 421 GGAGATGATGATGATCTTATTCAGGAGCAACCAATTAACCAACCATCAACATCATG 480
 Db 1268 GGAGATGATGATGATCTTATTCAGGAGCAACCAATTAACCAACCATCAACATCATG 1327
 QY 481 TTACAGAACTCTTCAGGAATAGAGAAATACAAAT 514
 Db 1328 TTACAGAACTCTTCAGGAATAGAGAAATACAAAT 1361

RESULT 2
 AA52357
 ID AAA52357 standard; cDNA; 1361 BP.
 XX
 AC AA52357;
 XX
 DT 18-SEP-2000 (first entry)
 XX
 DE cDNA encoding human low density lipoprotein-associated phospholipase A2.
 XX
 KW Human; low density lipoprotein associated phospholipase A2; LDL-PLA2;
 KW plasma PAF acetyl hydroxylase; recombinant; purification;
 KW short chain phospholipid; serine-dependent phospholipase; inflammation;
 KW proinflammatory; anti inflammatory; drug screening; antibody; diagnosis;
 KW ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 38..1360
 FT /tag= a
 FT /partial
 FT /product= "Human LDL-PLA2"
 FT

Query Match 100.0%; Score 514; DB 3; Length 1361;
 Best Local Similarity 100.0%; Pred. No. 2.5e-129;
 Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGACATTCCTTTGGTGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAGATTTCAGA 60
 Db 848 GGACATTCCTTTGGTGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAGATTTCAGA 907
 QY 61 TGTGGTATTCGCCCTGGATGCATGATGTTTCCACTGGGTGATGAAGTATATTCAGAAATT 120
 Db 908 TGTGGTATTCGCCCTGGATGCATGATGTTTCCACTGGGTGATGAAGTATATTCAGAAATT 967
 QY 121 CCTCAGCCCTCTTTTTCATCAACTCTGAATATTTCCAAATATCTGCTAATATCATATAAA 180
 Db 968 CCTCAGCCCTCTTTTTCATCAACTCTGAATATTTCCAAATATCTGCTAATATCATATAAA 1027
 QY 181 ATGAAAAATGCTACTCACCTGATPAAAGAAAGAGATGATTACAATCAGGGGTTTCAGTC 240
 Db 1028 ATGAAAAATGCTACTCACCTGATPAAAGAAAGAGATGATTACAATCAGGGGTTTCAGTC 1087
 QY 241 CACCGAATTTTGGTGCATCTTTCACCTTTGGCACTGGGCAAAATATTCGACATGCTCAAA 300
 Db 1088 CACCGAATTTTGGTGCATCTTTCACCTTTGGCACTGGGCAAAATATTCGACATGCTCAAA 1147
 QY 301 TTAAGGAGACATAGATTCAATGACAGTATTGATCTTAGCAACAAGCTTCATTAGCA 360
 Db 1148 TTAAGGAGACATAGATTCAATGACAGTATTGATCTTAGCAACAAGCTTCATTAGCA 1207
 QY 361 TTCTTACAAAAGCATTTAGGACTTCATAAAGATTTTCATCAGTGGGACTGCTGATTGAA 420
 Db 1208 TTCTTACAAAAGCATTTAGGACTTCATAAAGATTTTCATCAGTGGGACTGCTGATTGAA 1267
 QY 421 GGAGATGATGATGATCTTATTCAGGAGCAACCAATTAACCAACCATCAACATCATG 480
 Db 1268 GGAGATGATGATGATCTTATTCAGGAGCAACCAATTAACCAACCATCAACATCATG 1327
 QY 481 TTACAGAACTCTTCAGGAATAGAGAAATACAAAT 514
 Db 1328 TTACAGAACTCTTCAGGAATAGAGAAATACAAAT 1361

/note= "No stop codon given in the specification"

WO200024910-A1.
 04-MAY-2000.
 27-OCT-1999; 99WO-GB003551.
 28-OCT-1998; 98GB-00023647.
 28-OCT-1998; 98GB-00023648.
 (SMIK) SMITHKLINE BEECHAM PLC.

Boyd H, Tew DG;
 WPI; 2000-350749/30.
 P-PSDB; AAB01942.

Recombinant low density lipoprotein associated phospholipase A2, used to produce antibodies for diagnostics, is purified using a Blue Sepharose and Q Sepharose column.

Claim 6d; Page 15-17; 28pp; English.

The present sequence represents cDNA encoding human LDL-PLA2. The invention relates to a method for purifying recombinant low density lipoprotein-associated phospholipase A2 (LDL-PLA2). The method comprises applying a cell extract, supernatant or solution containing the recombinantly expressed LDL-PLA2 to a zinc chelating column, applying the eluate to a Blue Sepharose column, and applying that eluate to a Q Sepharose column. The invention also provides a process which additionally comprises the prior steps of constructing a vector comprising a cDNA encoding a histidine tagged LDL-PLA2 or fragment thereof, expressing the tagged protein in a host cell, isolating the tagged protein from the harvest medium or cell lysate, purifying the protein using a metal matrix affinity column (preferably a nickel column), and removing the histidine tag by protease cleavage. LDL-PLA2, also known as plasma PAF acetyl hydroxylase, is a serine-dependent phospholipase which catalyses the hydrolysis of phospholipids with short chain acyl groups at the sn-2 position. Its in vivo role is not known - due to its ability to hydrolyse both phospholipids with short chain an-2 substituents (which often arise from oxidative cleavage of longer chain sn-2 substituents) and PAF, it may be either a pro-inflammatory enzyme or an anti-inflammatory enzyme, depending on the precise in vivo role adopted. LDL-PLA2 can be used in structural and mechanistic studies to elucidate the activity of the enzyme in vivo. The enzyme may be used to screen and identify compounds which modulate its activity, and to raise antibodies for use in diagnostics

Sequence 1361 BP; 417 A; 273 C; 278 G; 393 T; 0 U; 0 Other;

Db 1088 CACCAGAAATTTTGCTGACTTCACCTTTTGCACCTGCGCAAAATAATTTGGACACATGCTCAAA 1147
Qy 301 TTAAGGAGACATAGATTCAAAATGCGACTATTGATCTTAGCAACAAAGCTTCATTAGCA 360
Db 1148 TTAAGGAGACATAGATTCAAAATGCGACTATTGATCTTAGCAACAAAGCTTCATTAGCA 1207
Qy 361 TTCTTACAAAGCAATTTAGGACTTCATAAAGATTTTGGATCAGTGGAGCTGCTTGAATGAA 420
Db 1208 TTCTTACAAAGCAATTTAGGACTTCATAAAGATTTTGGATCAGTGGAGCTGCTTGAATGAA 1267
Qy 421 CGAGATGATGAGAATCTTATTCCAGGACCAACATTAACACAACTCAACATCATG 480
Db 1268 CGAGATGATGAGAATCTTATTCCAGGACCAACATTAACACAACTCAACATCATG 1327
Qy 481 TTACAGAACTCTTCAGGAATAGAGAAATACAAAT 514
Db 1328 TTACAGAACTCTTCAGGAATAGAGAAATACAAAT 1361

RESULT 3

ABL67659
ID ABL67659 standard; DNA; 1561 BP.
XX AC ABL67659;
XX XX
XX 15-MAY-2002 (first entry)
XX Oesophagus cancer related gene sequence SEQ ID NO:5996.
XX Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KW cystostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
KW gene; ds.
XX OS Homo sapiens.
XX PN WO200194629-A2.
XX PD 13-DEC-2001.
XX PF 30-MAY-2001; 2001WO-US010838.
XX XX

PR 05-JUN-2000; 2000US-0209473P.
PR 05-JUN-2000; 2000US-0209531P.
PR 18-SEP-2000; 2000US-0233133P.
PR 18-SEP-2000; 2000US-0233617P.
PR 20-SEP-2000; 2000US-0234009P.
PR 20-SEP-2000; 2000US-0234034P.
PR 20-SEP-2000; 2000US-0234052P.
PR 22-SEP-2000; 2000US-0234509P.
PR 22-SEP-2000; 2000US-0234567P.
PR 25-SEP-2000; 2000US-0234923P.
PR 25-SEP-2000; 2000US-0234924P.
PR 25-SEP-2000; 2000US-0235077P.
PR 25-SEP-2000; 2000US-0235082P.
PR 25-SEP-2000; 2000US-0235134P.
PR 26-SEP-2000; 2000US-0235280P.
PR 26-SEP-2000; 2000US-0235637P.
PR 26-SEP-2000; 2000US-0235638P.
PR 27-SEP-2000; 2000US-0235711P.
PR 27-SEP-2000; 2000US-0235720P.
PR 27-SEP-2000; 2000US-0235840P.
PR 27-SEP-2000; 2000US-0235863P.
PR 28-SEP-2000; 2000US-0236028P.
PR 28-SEP-2000; 2000US-0236032P.
PR 28-SEP-2000; 2000US-0236033P.
PR 28-SEP-2000; 2000US-0236034P.
PR 28-SEP-2000; 2000US-0236103P.
PR 28-SEP-2000; 2000US-0236111P.
PR 29-SEP-2000; 2000US-0236842P.
PR 29-SEP-2000; 2000US-0236891P.
PR 02-OCT-2000; 2000US-0237172P.
PR 02-OCT-2000; 2000US-0237173P.

PR 02-OCT-2000; 2000US-0237278P.
PR 02-OCT-2000; 2000US-0237294P.
PR 02-OCT-2000; 2000US-0237295P.
PR 02-OCT-2000; 2000US-0237316P.
PR 03-OCT-2000; 2000US-0237425P.
PR 03-OCT-2000; 2000US-0237598P.
PR 03-OCT-2000; 2000US-0237604P.
PR 03-OCT-2000; 2000US-0237606P.
PR 03-OCT-2000; 2000US-0237608P.
PR 01-NOV-2000; 2000US-0244867P.
PR 01-NOV-2000; 2000US-0245084P.
XX XX
XX (AVAL-) AVALON PHARM.
XX Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
XX Soppet DR, Weaver Z;
XX WPI; 2002-188264/24.

Screening for anti-neoplastic agent involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, and determining a change in expression of a gene of a signature gene set.

Claim 1; SEQ ID NO 5996; 44pp; English.

The present invention describes a method (M1) for screening for an anti-neoplastic agent. The method involves exposing cells to a chemical agent to be tested for anti-neoplastic activity, determining a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 8447 sequences (given in ABL61664 to ABL70110), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. M1 can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of M1, and the data is sufficient to convey the chemical structure and/or properties of the agent. M1 can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney, prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's tumour

XX SQ Sequence 1561 BP; 447 A; 337 C; 352 G; 425 T; 0 U; 0 Other;

Query Match 100.0%; Score 514; DB 6; Length 1561;

Best Local Similarity 100.0%; Pred. No. 2.6e-129;

Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGACATCTTTTGTGGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAGATTGAGA 60
Db 1027 GGACATCTTTTGTGGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAGATTGAGA 1086
Qy 61 TGTGTTATTCCTGGATGCATGGATGTTTCCACTGGGTGATGAAGTATATTCAGAAATT 120
Db 1087 TGTGTTATTCCTGGATGCATGGATGTTTCCACTGGGTGATGAAGTATATTCAGAAATT 1146
Qy 121 CCTCAGCCCTCTTTTATCAACTCTGAATATTTTCAATATCTCTGCTAATATCAATAAA 180
Db 1147 CCTCAGCCCTCTTTTATCAACTCTGAATATTTTCAATATCTCTGCTAATATCAATAAA 1206
Qy 181 ATGAAAAATGCTACTACCTGTATAAGAAAGAAAGATGATACATCAGGGTTGAGTC 240
Db 1207 ATGAAAAATGCTACTACCTGTATAAGAAAGAAAGATGATGATCAATCAGGGTTGAGTC 1266
Qy 241 CACCAGAAATTTGCTGACTTCACCTTTTGCACCTTTCGCACTGCAAAATAATTTGGACACATGCTCAAA 300
Db 1267 CACCAGAAATTTGCTGACTTCACCTTTTGCACCTTTCGCACTGCAAAATAATTTGGACACATGCTCAAA 1326
Qy 301 TTAAGGGAGACATAGATTCAAATGCAGCTATTGATCTTAGCAACAAAGCTTCATTAGCA 360
Db 1327 TTAAGGGAGACATAGATTCAAATGCAGCTATTGATCTTAGCAACAAAGCTTCATTAGCA 1386

QY 361 TTCTTACAAAGCAATTTAGGACTTCATTAAGATTTTGAATCAGTGGGACTGCTTGAATGAA 420
 Db 1387 TTCTTACAAAGCAATTTAGGACTTCATTAAGATTTTGAATCAGTGGGACTGCTTGAATGAA 1446
 QY 421 GGAGATGATGAGATCTTATTCCAGGGACCAACATTAACACCAATCAACACATCATG 480
 Db 1447 GGAGATGATGAGATCTTATTCCAGGGACCAACATTAACACCAATCAACACATCATG 1506
 QY 481 TTACAGAACTCTTCAGGAATAGAGAAATACAAAT 514
 Db 1507 TTACAGAACTCTTCAGGAATAGAGAAATACAAAT 1540

RESULT 4

AAD36733
 ID AAD36733 standard; cDNA; 1323 BP.
 XX AC AAD36733;
 XX DT 04-OCT-2002 (first entry)
 XX DE Human lipoprotein-associated phospholipase A2 cDNA.
 XX KW Atherosclerosis; single nucleotide polymorphism; SNP;
 KW Lipoprotein-associated phospholipase A2; Lp-PLA2; human; ss.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 XX FT 1..1323
 FT /*tag= a
 FT /product= "Lipoprotein-associated phospholipase A2"
 FT /note= "Does not include stop codon"
 FT /partial
 FT variation replace(1136, T)
 FT /*tag= b
 FT /standard_name= "Single nucleotide polymorphism (SNP)"
 FT /note= "This SNP brings about amino acid change of Ala to Val"
 XX WO200236817-A2.
 XX 10-MAY-2002.
 XX 02-NOV-2001; 2001WO-GB004876.
 XX 04-NOV-2000; 2000GB-00027181.
 XX (SMIK) SMITHKLINE BEECHAM PLC.
 XX Campbell D, McGinnins R, Spurr N, Valdes AM;
 XX WPI; 2002-479764/51.
 XX P-PSDB; AAE14750.
 XX Diagnosing atherosclerosis or predicting susceptibility of a subject to atherosclerosis by determining single nucleotide polymorphism in Lp-PLA2-encoding polynucleotide.
 XX Claim 3; Page 14; 30pp; English.

XX The invention relates to a method of diagnosing atherosclerosis or predicting the susceptibility of a subject to atherosclerosis, comprising determining the presence or absence of a single nucleotide polymorphism (SNP) in codon 379 of a lipoprotein-associated phospholipase A2 (Lp-PLA2)-encoding polynucleotide, where the codon comprising the SNP encodes an amino acid other than valine. The method is useful for predicting the likelihood of developing atherosclerosis, predicting and responding to the progression of the atherosclerotic condition and drug treatment, or predicting disease outcome in a subject. The method is also useful in the selection of patient groups for conducting clinical trials concerning therapeutic compounds with potential for use in the treatment of atherosclerosis. The present sequence is human lipoprotein-associated

CC phospholipase A2 cDNA
 XX Sequence 1323 BP; 406 A; 263 C; 269 G; 385 T; 0 U; 0 Other;
 SQ
 Query Match. 99.8%; Score 513; DB 6; Length 1323;
 Best Local Similarity 100.0%; Pred. No. 4.6e-129;
 Matches 513; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGACATTTCTTTGGTGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAGATTGAGA 60
 Db 811 GGACATTTCTTTGGTGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAGATTGAGA 870
 QY 61 TGTGTTATTCCTCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120
 Db 871 TGTGTTATTCCTCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 930
 QY 121 CCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAAATATCTCTGCTAATATCATATAA 180
 Db 931 CCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAAATATCTCTGCTAATATCATATAA 990
 QY 181 ATGAAAAAATGCTACTCACCTGATAAAGAAAGAAAGATGATTACAATCAGGGGTTGAGTC 240
 Db 991 ATGAAAAAATGCTACTCACCTGATAAAGAAAGAAAGATGATTACAATCAGGGGTTGAGTC 1050
 QY 241 CACCAGAAATTTGCTGACTTCACTTTTGGCAACTGGCAAAATAATTGGACACATGCTCAAA 300
 Db 1051 CACCAGAAATTTGCTGACTTCACTTTTGGCAACTGGCAAAATAATTGGACACATGCTCAAA 1110
 QY 301 TTAAGGAGACATAGATTCAAAATGAGCTATTGATCTTAGCAACCAAGCTTCATTAGCA 360
 Db 1111 TTAAGGAGACATAGATTCAAAATGAGCTATTGATCTTAGCAACCAAGCTTCATTAGCA 1170
 QY 361 TTCTTACAAAAGCAATTTAGGACTTTCATAAAGATTTTGGATCAGTGGGACTGCTTGAATGAA 420
 Db 1171 TTCTTACAAAAGCAATTTAGGACTTTCATAAAGATTTTGGATCAGTGGGACTGCTTGAATGAA 1230
 QY 421 GGAGATGATGAGATCTTATTTCAGGGACCAACATTAACACCAATCAACACATCATG 480
 Db 1231 GGAGATGATGAGATCTTATTTCAGGGACCAACATTAACACCAATCAACACATCATG 1290
 QY 481 TTACAGAACTCTTCAGGAATAGAGAAATACAAAT 513
 Db 1291 TTACAGAACTCTTCAGGAATAGAGAAATACAAAT 1323
 RESULT 5
 ID ADG73659 standard; DNA; 1203 BP.
 XX AC ADG73659;
 XX DT 11-MAR-2004 (first entry)
 XX DE Human PAF-AH gene SEQ ID NO:7.
 KW ds; gene; collagenase; collagen; platelet activating factor;
 KW acetyl hydrolase; collagen coupling region; antiinflammatory;
 KW inflammation; skin transplantation; human.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 XX FT 1..1203
 FT /*tag= a
 FT /product= "PAF-AH"
 FT /note= "No start codon given"
 XX JP2003284553-A.
 XX 07-OCT-2003.
 XX 28-MAR-2002; 2002JP-00090847.
 XX

Db 1111 TTAAGGGAGACATAGATTTCAATGTAGCTATTGATCTTAGCAACAAGCTTCTATTAGCA 1170
 Qy 361 TTCTTACAAAAGCATTTAGGACTTCATAAAGATTTTCATCAGTGGGACTGCTTGAATGAA 420
 Db 1171 TTCTTACAAAAGCATTTAGGACTTCATAAAGATTTTCATCAGTGGGACTGCTTGAATGAA 1230
 Qy 421 GGAGATGATGAGATCTTTATTCAGGAGCAACCAATTAACCAACCAATCAACATCATG 480
 Db 1231 GGAGATGATGAGATCTTTATTCAGGAGCAACCAATTAACCAACCAATCAACATCATG 1290
 Qy 481 TTACAGAACTCTTCAGGAATAGAGAAATCAATTT 514
 Db 1291 TTACAGAACTCTTCAGGAATAGAGAAATCAATTT 1324

RESULT 7

AA10885
 ID AA10885 standard; cDNA; 1335 BP.

XX AC AA10885;

XX DT 14-JUL-2000 (first entry)

XX DE Synthetic PAF-AH coding sequence used in PAF-AH construct.

XX KW Platelet-activating factor acetyl hydrolase; PAF-AH; PAF; phospholipid;
 inflammatory response; pre-term labour; pharmaceutical composition;
 regulate; asthma; anaphylaxis; shock; arthritis; Crohn's disease; ss;
 pancreatitis; allergic inflammation; human immunodeficiency virus; HIV.

XX OS Synthetic.

XX XX US6045794-A.

XX XX 04-APR-2000.

XX XX 09-JUN-1999; 99US-00328474.

XX XX 06-OCT-1993; 93US-00133803.

XX XX 06-OCT-1994; 94US-00318905.

XX XX 07-JUN-1995; 95US-00483232.

XX XX 12-AUG-1997; 97US-00910041.

XX XX (ICOS-) ICOS CORP.

XX XX Cousins LS, Gray P, Trong HL, Tjoelker LW, Wilder CJ;

XX XX Eberhardt CD;

XX XX WPI; 2000-282671/24.

XX XX Treatment of mammals suffering from pre-term labor comprises

XX XX administering a pharmaceutical composition comprising platelet-activating

XX XX factor acetyl hydrolase enzyme.

XX XX Example 8; Col 99-102; 67pp; English.

XX XX This sequence represents a recoded nucleotide sequence encoding platelet-
 activating factor acetyl hydrolase (PAF-AH). PAF is a phospholipid and is
 implicated in pathological inflammatory responses (e.g. asthma,
 anaphylaxis, septic shock and arthritis). PAF-AH is released by
 hepatocytes, and macrophages and inactivates PAF. PAF-AH also inactivates
 oxidatively fragmented phospholipids that mediate inflammation. The human
 PAF-AH nucleotide and protein sequences (see AA10861 and AA98301) is
 specifically claimed for use in a method to treat a mammal suffering from
 pre-term labour. PAF-AH is included in a pharmaceutical composition which
 can be administered to a mammal suffering from pre-term labour. The
 invention relates to purified and isolated polynucleotide sequences
 encoding human PAF-AH and materials and methods for the recombinant
 production of PAF-AH products which are expected to be useful in
 regulating inflammatory events. The administration of PAF-AH to animals
 may be used for ameliorating pathological inflammatory conditions such as
 asthma, anaphylaxis, shock, arthritis, Crohn's disease, pancreatitis,

CC allergic inflammation, and human immunodeficiency virus (HIV)
 XX SQ Sequence 1335 BP; 406 A; 277 C; 286 G; 366 T; 0 U; 0 Other;

Query Match 99.7%; Score 512.4; DB 3; Length 1335;
 Best Local Similarity 99.8%; Pred. No. 6.7e-129;
 Matches 513; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGACATCTTTTGGTGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAGATTTCAGA 60
 Db 811 GGACATCTTTTGGTGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAGATTTCAGA 870
 Qy 61 TGTGGTATTGCCCTGGATGCATGGATGTTTCCACTGGTGGTGAATATTCAGAAATT 120
 Db 871 TGTGGTATTGCCCTGGATGCATGGATGTTTCCACTGGTGGTGAATATTCAGAAATT 930
 Qy 121 CCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAAATATCTCTGCTAATATCAATAA 180
 Db 931 CCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAAATATCTCTGCTAATATCAATAA 990
 Qy 181 ATGAAAAAATGCTACTCACCTGATAAAGAAAGATGATTACAATCAGGGGTTCAAGTC 240
 Db 991 ATGAAAAAATGCTACTCACCTGATAAAGAAAGATGATTACAATCAGGGGTTCAAGTC 1050
 Qy 241 CACCAGAAATTTGCTGACTCTTCTTGGCAACTGGCAAAATAATGGACACATGCTCAAA 300
 Db 1051 CACCAGAAATTTGCTGACTCTTCTTGGCAACTGGCAAAATAATGGACACATGCTCAAA 1110
 Qy 301 TTAAGGGAGACATAGATTTCAATGAGCTTATTGATCTTAGCAACAAGCTTCAATAGCA 360
 Db 1111 TTAAGGGAGACATAGATTTCAATGAGCTTATTGATCTTAGCAACAAGCTTCAATAGCA 1170
 Qy 361 TTCTTACAAAAGCATTTAGGACTTCATAAAGATTTTTCAGTGGGACTCTTGAATGAA 420
 Db 1171 TTCTTACAAAAGCATTTAGGACTTCATAAAGATTTTTCAGTGGGACTCTTGAATGAA 1230
 Qy 421 GGAGATGATGAGAAATCTTATTCAGGGACCAACATTAACCAACCAATCAACATCATG 480
 Db 1231 GGAGATGATGAGAAATCTTATTCAGGGACCAACATTAACCAACCAATCAACATCATG 1290
 Qy 481 TTACAGAACTCTTCAGGAATAGAGAAATCAATTT 514
 Db 1291 TTACAGAACTCTTCAGGAATAGAGAAATCAATTT 1324

RESULT 8

AA224261

ID AA224261 standard; cDNA; 1335 BP.

XX AC AA224261;

XX DT 08-FEB-2000 (first entry)

XX DE Human PAF-AH cDNA fragment.

XX XX

XX KW Platelet activating factor acetylhydrolase; PAF-AH; human; treatment;
 antiinflammatory; antiasthmatic; antiallergic; antiarthritic; asthma;
 antiischemic; inflammatory disorder; anaphylaxis; ulcerative colitis;
 antigen-induced arthritis; ischemia; septicemia; allergy; ss.

XX OS Homo sapiens.

XX PN US5977308-A.

XX XX 02-NOV-1999.

XX PF 12-AUG-1997; 97US-00910041.

XX XX 06-OCT-1993; 93US-00133803.

XX PR 06-OCT-1994; 94US-00318905.

XX PR 07-JUN-1995; 95US-00483232.

XX XX (ICOS-) ICOS CORP.

XX Cousins LS, Gray P, Trong HL, Tjoelker LW, Wilder CL;
PI Eberhardt CD;
XX WPI; 2000-021956/02.
XX Truncated and substituted versions of human platelet activating factor
PT acetylhydrolase, for treating or preventing inflammatory diseases such as
PT asthma.
XX Example 8; Col 95-98; 65pp; English.
XX This invention describes novel truncated and variant forms (I) of human
CC PAF-AH (platelet activating factor acetylhydrolase) which have
CC antiinflammatory, antiasthmatic, antiallergic, antiarthritic and
CC antileukemic activity. (I) are used to treat a wide variety of
CC inflammatory disorders, e.g. asthma, anaphylaxis, antigen-induced
CC arthritis, ulcerative colitis, ischemia, septicemia, allergy, etc.
CC Recombinant (I), produced in prokaryotic cells, are less heterogeneous at
CC the termini than the full-length protein. Some of the truncated versions
CC also have greater activity than the wild-type enzyme. This sequence
CC represents a human PAF-AH DNA fragment which is used in the construction
CC of plasmid pRC/HPH.4
XX
SQ Sequence 1335 BP; 406 A; 277 C; 286 G; 366 T; 0 U; 0 Other;
Query Match 99.7%; Score 512.4; DB 3; Length 1335;
Best Local Similarity 99.8%; Pred. No. 6.7e-129;
Matches 513; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GGACATTCCTTTTGGTGAGCAACGGTTATTCAGACTCTTAGTGAAGATCAGAGATTTCAGA 60
Db 811 GGACATTCCTTTTGGTGAGCAACGGTTATTCAGACTCTTAGTGAAGATCAGAGATTTCAGA 870
Qy 61 TGTGGTATTCCTCGGATGCATGATGTTTCCACTGGTGATGAAGTATATTCAGAAATT 120
Db 871 TGTGGTATTCCTCGGATGCATGATGTTTCCACTGGTGATGAAGTATATTCAGAAATT 930
Qy 121 CCTCAGCCCTCTTTTATCAACTCTGAATATTCCTCAATATCTGCTAATATCAATAAAA 180
Db 931 CCTCAGCCCTCTTTTATCAACTCTGAATATTCCTCAATATCTGCTAATATCAATAAAA 990
Qy 181 ATGAAAATGCTACTCACCTGATAAAGAAAGAAAGATGATTACAATCAGGGTTTCAGTC 240
Db 991 ATGAAAATGCTACTCACCTGATAAAGAAAGAAAGATGATTACAATCAGGGTTTCAGTC 1050
Qy 241 CACCAGAAATTTGCTGACTTCACTTTGCACTGGCAAAATAATTTGGACACATGCTCAAA 300
Db 1051 CACCAGAAATTTGCTGACTTCACTTTGCACTGGCAAAATAATTTGGACACATGCTCAAA 1110
Qy 301 TTAAGGGAGACATAGATTCAAAATGCACTATTGATCTTAGCAACAAAGCTTCATTAGCA 360
Db 1111 TTAAGGGAGACATAGATTCAAAATGCTAGTATTGATCTTAGCAACAAAGCTTCATTAGCA 1170
Qy 361 TTCTTACAAAGCAATTTAGGACTTCATAAGATTTTGAATGAGTGGAGCTGCTTGAATGAA 420
Db 1171 TTCTTACAAAGCAATTTAGGACTTCATAAGATTTTGAATGAGTGGAGCTGCTTGAATGAA 1230
Qy 421 GGAGATGATGAGATCTTATTTCAGGAGCAACCAATTAACCAACCAATCAACATCATG 480
Db 1231 GGAGATGATGAGATCTTATTTCAGGAGCAACCAATTAACCAACCAATCAACATCATG 1290
Qy 481 TTACAGAACTCTTCAGGAATAGAGAAATACAAATT 514
Db 1291 TTACAGAACTCTTCAGGAATAGAGAAATACAAATT 1324
RESULT 9
AAD04165
ID AAD04165 standard; DNA; 1335 BP.
XX
AC AAD04165;
XX

DT 02-JUL-2001 (first entry)
DE Human plasma platelet-activating factor (PAF)-AH recoded gene.
XX
KW Human; platelet-activating factor acetylhydrolase; PAF-AH; arthritis;
KW antiinflammatory; septicemia; inflammation; haemostasis; parturition;
KW asthma; anaphylaxis; septic shock; antibacterial; ds.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN US6203790-B1.
XX
XX 20-MAR-2001.
PD
XX 23-MAY-2000; 2000US-00577758.
XX
XX 06-OCT-1993; 93US-00133803.
PR 06-OCT-1994; 94US-00318905.
PR 07-JUN-1995; 95US-00480658.
PR 22-JAN-1998; 98US-00010715.
XX
XX (ICOS-) ICOS CORP.
XX
XX Cousins LS, Eberhardt CD, Gray P, Trong HL, Tjoelker LW;
PI Wilder CL;
XX
XX WPI; 2001-280610/29.
DR
XX
XX Treating a mammal susceptible to or suffering from septicemia comprises
PT administering a platelet-activating factor acetyl hydrolase (PAF-AH) to
PT supplement endogenous PAF-AH activity and to inactivate pathological
PT amounts of PAF.
XX
XX Example 8; Col 79-80; 54pp; English.
XX
XX The present DNA sequence is human plasma platelet-activating factor.
CC acetylhydrolase (PAF-AH) recoded gene. First 290 bases of the PAF-AH
CC coding sequence was recoded, in which most of the codons have been
CC substituted with a codon of different sequence but encoding the same
CC amino acid was constructed. This recoded gene is successful in boosting
CC the expression levels of human PAF-AH from a few nanograms/ml to about
CC 0.5 microgram/ml in a transient COS cell transfection system. The
CC invention relates to human plasma platelet-activating factor
CC acetylhydrolase (PAF-AH) and its corresponding cDNA molecule. The
CC invention also relates to method of treating a mammal susceptible to or
CC suffering from septicemia. PAF functions in normal physiological
CC processes such as inflammation, haemostasis and parturition. PAF-AH
CC specific antibodies are used in the diagnostic methods to detect abnormal
CC levels of PAF-AH in serum and also for treating the pathological
CC inflammatory conditions of PAF-AH such as asthma, anaphylaxis, septic
CC shock and arthritis. PAF-AH antibody is also useful for screening a
CC genetic lesion in the human plasma PAF-AH gene, which occurs due to the
CC replacement of nucleotide G to T at position 996 within exon 9 resulting
CC in replacement of amino acid Val to Phe at position 279. Thus the
CC deficiency of PAF-AH activity is due to the genetic lesion in human
CC plasma PAF-AH gene
XX
SQ Sequence 1335 BP; 406 A; 277 C; 286 G; 366 T; 0 U; 0 Other;
Query Match 99.7%; Score 512.4; DB 4; Length 1335;
Best Local Similarity 99.8%; Pred. No. 6.7e-129;
Matches 513; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GGACATTCCTTTTGGTGAGCAACGGTTATTCAGACTCTTAGTGAAGATCAGAGATTTCAGA 60
Db 811 GGACATTCCTTTTGGTGAGCAACGGTTATTCAGACTCTTAGTGAAGATCAGAGATTTCAGA 870
Qy 61 TGTGGTATTCCTCGGATGCATGATGTTTCCACTGGTGATGAAGTATATTCAGAAATT 120
Db 871 TGTGGTATTCCTCGGATGCATGATGTTTCCACTGGTGATGAAGTATATTCAGAAATT 930
Qy 121 TGTGGTATTCCTCGGATGCATGATGTTTCCACTGGTGATGAAGTATATTCAGAAATT 930
Db 871 TGTGGTATTCCTCGGATGCATGATGTTTCCACTGGTGATGAAGTATATTCAGAAATT 930
Qy 121 CCTCAGCCCTCTTTTATCAACTCTGAATATTCCTCAATATCTGCTAATATCAATAAAA 180

Db 812 GGACATCTCTTTTGGTGAGCAACGGTTATTTCAGACTCTTAGTGAGATCAGAGATTTCAGA 871
 Qy 61 TGTGGTATTCCTCGGATGATGATGTTTCCACTGGGTGATGAAGTATATTCAGAAATT 120
 Db 872 TGTGGTATTCCTCGGATGATGATGTTTCCACTGGGTGATGAAGTATATTCAGAAATT 931
 Qy 121 CCTCAGCCCTCTCTTTTATCACTCTGAATATTCGAATATCTGCTTAATATCATATAA 180
 Db 932 CCTCAGCCCTCTCTTTTATCACTCTGAATATTCGAATATCTGCTTAATATCATATAA 991
 Qy 181 ATGAAAAAATCTACTCACCTGATAAAGAAAGAGATGATTACAATCAGGGTTCAGTC 240
 Db 992 ATGAAAAAATCTACTCACCTGATAAAGAAAGAGATGATTACAATCAGGGTTCAGTC 1051
 Qy 241 CACCAGAAATTTGCTGACTTTCACCTTTTGCACTGGCAAAATAATTGGACACATCTCAAA 300
 Db 1052 CACCAGAAATTTGCTGACTTTCACCTTTTGCACTGGCAAAATAATTGGACACATCTCAAA 1111
 Qy 301 TTAAGGGAGACATAGATTCAATGCGACTTATTGATCTTAGCAACAAAGCTTCATTAGCA 360
 Db 1112 TTAAGGGAGACATAGATTCAATGCGACTTATTGATCTTAGCAACAAAGCTTCATTAGCA 1171
 Qy 361 TTCTTTACAAAAGCATTTAGGACTTCATAAAGATTTTTCATCAGTGGAGCTGCTTGAATGAA 420
 Db 1172 TTCTTTACAAAAGCATTTAGGACTTCATAAAGATTTTTCATCAGTGGAGCTGCTTGAATGAA 1231
 Qy 421 GGAGATGATGAGATCTTATTTCAGGGACCAACATTAACCAACCAATCAACATCATG 480
 Db 1232 GGAGATGATGAGATCTTATTTCAGGGACCAACATTAACCAACCAATCAACATCATG 1291
 Qy 481 TTACAGAACTCTTCAGGAATAGAGAAATACAAATT 514
 Db 1292 TTACAGAACTCTTCAGGAATAGAGAAATACAAATT 1325

RESULT 13

ABK92177

ID ABK92177 standard; DNA; 1505 BP.

XX

AC ABK92177;

XX 15-AUG-2002 (first entry)

DE Prostate cancer-associated DNA sequence #63.

XX Prostate cancer; prostate tumour tissue; human; mammal; cytostatic;
 KW gene therapy; gene; ds.

XX Mammalia.

XX W0200230268-A2.

XX 18-APR-2002.

XX 12-OCT-2001; 2001WO-US032045.

XX 13-OCT-2000; 2000US-00687576.

PR 08-DEC-2000; 2000US-00733288.

PR 08-DEC-2000; 2000US-00733742.

PR 24-JAN-2001; 2001US-0263957P.

PR 16-MAR-2001; 2001US-0276791P.

PR 16-MAR-2001; 2001US-0276888P.

PR 06-APR-2001; 2001US-0281922P.

PR 24-APR-2001; 2001US-0286214P.

PR 30-APR-2001; 2001US-00847046.

PR 04-MAY-2001; 2001US-0288589P.

XX (EOSB-) EOS BIOTECHNOLOGY INC.

XX Gish KC, Mack DH, Wilson KE, Afar D, Hevezi P;

XX WPI; 2002-471335/50.

XX P-PSDB; ABG61862.

DR

XX

PT Detecting a prostate cancer-associated transcript in a cell in a patient,
 PT useful for diagnosing prostate cancer (PC) or screening modulators of PC,
 PT by determining if prostate cancer-associated genes are expressed in a
 PT prostate tissue.

XX

Claim 22; Page 347; 436pp; English.

XX

PS The present invention relates to methods of detecting a prostate cancer-
 PS associated transcript in a cell from a patient. The method comprises
 CC contacting a biological sample from the patient with prostate cancer-
 CC associated polynucleotides (designated PC genes) that selectively
 CC hybridise to a sequence that is at least 80% identical to them. The
 CC prostate cancer-associated polynucleotide sequences are differentially
 CC expressed in prostate tumour tissue or in prostate cancer and are derived
 CC from the tissues of various organisms such as humans or other mammals
 CC (e.g. mice, sheep and dogs). The methods of the invention are useful for
 CC diagnosing and treating prostate cancer in mammals. The prostate cancer-
 CC associated genes are useful for diagnosing or treating prostate cancer,
 CC as well as for identifying modulators of prostate cancer or agents that
 CC inhibit prostate cancer. The nucleic acid sequences are particularly
 CC useful in gene therapy, as a vaccine or in antisense applications.
 CC ABK92115-ABK92263 represent prostate cancer-associated polynucleotide
 CC sequences

XX

SQ Sequence 1505 BP; 438 A; 311 C; 333 G; 423 T; 0 U; 0 Other;

Query Match

99.7%; Score 512.4; DB 6; Length 1505;

Best Local Similarity 99.8%; Pred. No. 7e-129;

Matches 513; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy

1 GGACATCTCTTTTGGTGAGCAACGGTTATTTCAGACTCTTAGTGAGATCAGAGATTTCAGA 60

Db

972 GGACATCTCTTTTGGTGAGCAACGGTTATTTCAGACTCTTAGTGAGATCAGAGATTTCAGA 1031

Qy

61 TGTGGTATTCCTCGGATGATGATGTTTCCACTGGGTGATGAAGTATATTCAGAAATT 120

Db

1032 TGTGGTATTCCTCGGATGATGATGTTTCCACTGGGTGATGAAGTATATTCAGAAATT 1091

Qy

121 CCTCAGCCCTCTCTTTTATCACTCTGAATATTTTCCAATATCTGCTTAATATCATATAA 180

Db

1092 CCTCAGCCCTCTCTTTTATCACTCTGAATATTTTCCAATATCTGCTTAATATCATATAA 1151

Qy

181 ATGAAAAAATGCTACTCACCTGATAAAGAAAGAGATGATTACAATCAGGGGTTCAGTC 240

Db

1152 ATGAAAAAATGCTACTCACCTGATAAAGAAAGAGATGATTACAATCAGGGGTTCAGTC 1211

Qy

241 CACCAGAAATTTGCTGACTTTCACCTTTTGCACTGGCAAAATAATTGGACACATGCTCAAA 300

Db

1212 CACCAGAAATTTGCTGACTTTCACCTTTTGCACTGGCAAAATAATTGGACACATGCTCAAA 1271

Qy

301 TTAAGGGAGACATAGATTCAAAATGCAGCTATTGTAGCTTAGCAACAAAGCTTCATTAGCA 360

Db

1272 TTAAGGGAGACATAGATTCAAAATGCAGCTATTGTAGCTTAGCAACAAAGCTTCATTAGCA 1331

Qy

361 TTCTTACAAAAGCATTTAGGACTTCATAAAGATTTTTCAGTGGGACTGCTTGAATGAA 420

Db

1332 TTCTTACAAAAGCATTTAGGACTTCATAAAGATTTTTCAGTGGGACTGCTTGAATGAA 1391

Qy

421 GGAGATGATGAGATCTTATTTCAGGGACCAACATTAACCAACCAATCAACATCATG 480

Db

1392 GGAGATGATGAGATCTTATTTCAGGGACCAACATTAACCAACCAATCAACATCATG 1451

Qy

481 TTACAGAACTCTTCAGGAATAGAGAAATACAAATT 514

Db

1452 TTACAGAACTCTTCAGGAATAGAGAAATACAAATT 1485

XX

RESULT 14

ADP64943

ID ADP64943

XX ADP64943 standard; DNA; 1505 BP.

XX

AC ADP64943;

XX	12-AUG-2004	(first entry)
DT	Human phospholipase A2, group VII (platelet-activating) DNA sequence.	
DE		
DE	autoimmune disease; arthritis; gene expression analysis;	
KW	rheumatoid arthritis; collagen-induced; immunosuppressive; antirheumatic;	
KW	antiarthritic; osteopathic; antigen; antiinflammatory; dermatological;	
KW	immunomodulatory; lupus; ankylosing spondylitis; fibrositis;	
KW	fibromyalgia; osteoarthritis; gout; juvenile rheumatoid arthritis;	
KW	immune; ds; human.	
OS	Homo sapiens.	
PN	WO2003072827-A1.	
XX		
PD	04-SEP-2003.	
XX		
PF	31-OCT-2002; 2002WO-US035433.	
XX		
PR	31-OCT-2001; 2001US-0336220P.	
PA	(CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.	
PI	Hirsch R, Thorton SL;	
DR	WPI; 2003-712740/67.	
DR	GENBANK; NM_005084.	
XX		
PT	Diagnosing and analyzing autoimmune disease using gene expression	
PT	profiles and microarray technology, useful for diagnosing and treating	
PT	rheumatoid arthritis, lupus, fibrositis, osteoarthritis, fibromyalgia and	
XX	gout.	
PS	Disclosure; Page; 56pp; English.	
XX		
CC	The invention relates to a novel method for diagnosing and analysing	
CC	autoimmune disease or arthritides. The method comprises obtaining a	
CC	patient sample containing mRNA, analysing gene expression using the mRNA	
CC	that results in a gene expression signature of the mRNA, and using that	
CC	gene expression signature to diagnose or analyse the autoimmune disease	
CC	or arthritides in the patient, where gene expression of at least 60% of	
CC	the genes correlates with that of the gene signature. The invention	
CC	further comprises: a treatment of rheumatoid arthritis; identification of	
CC	genes for targeting in the treatment of rheumatoid arthritis in a mammal	
CC	other than a mouse; diagnosis of rheumatoid arthritis in a mammal; an	
CC	array or gene chip, specific for rheumatoid arthritis; diagnosis or	
CC	analyses of autoimmune disease or rheumatoid arthritis; screening the	
CC	efficacy of a candidate drug in vitro for the treatment of collagen-	
CC	induced arthritis; and reducing the symptoms associated with collagen-	
CC	induced arthritis. The compositions of the invention have the following	
CC	activities: immunosuppressive, antirheumatic, antiarthritic, osteopathic,	
CC	antigout, antiinflammatory, dermatological, and immunomodulatory. The	
CC	methods and compositions of the present invention are useful for	
CC	diagnosing and treating autoimmune disease or arthritides, such as	
CC	rheumatoid arthritis, lupus, ankylosing spondylitis, fibrositis,	
CC	fibromyalgia, osteoarthritis, gout, juvenile rheumatoid arthritis, and an	
CC	immune disease caused by an infectious agent. This polynucleotide	
CC	represents a DNA sequence relating to the genes used in the analysis and	
CC	treatment of autoimmune diseases or arthritides. Note: This sequence is	
CC	not shown in the specification. It has been supplied in an electronic	
CC	format from WIPO.	
XX		
SQ	Sequence 1505 BP; 438 A; 311 C; 333 G; 423 T; 0 U; 0 Other;	
Query Match	99.7%; Score 512.4; DB 11; Length 1505;	
Best Local Similarity	99.8%; Pred. No. 7e-129;	
Matches 513; Conservative	0; Mismatches 1; Indels 0; Gaps 0;	
QY	1 GGACATCTTTTGGTGAGCAACGGTATTTCAGACTCTTAGTGAAGATCAGAGATTGAGA 60	
DB		
DB	972 GGACATCTTTTGGTGAGCAACGGTATTTCAGACTCTTAGTGAAGATCAGAGATTGAGA 1031	

XX The invention relates to a novel method for diagnosing and analysing
CC autoimmune disease or arthritides. The method comprises obtaining a
CC patient sample containing mRNA, analysing gene expression using the mRNA
CC that results in a gene expression signature of the mRNA, and using that
CC gene expression signature to diagnose or analyse the autoimmune disease
CC or arthritides in the patient, where gene expression of at least 60% of
CC the genes correlates with that of the gene signature. The invention
CC further comprises: a treatment of rheumatoid arthritis; identification of
CC genes for targeting in the treatment of rheumatoid arthritis in a mammal
CC other than a mouse; diagnosis of rheumatoid arthritis in a mammal; an
CC array or gene chip, specific for rheumatoid arthritis; diagnosis or
CC analyses of autoimmune disease or rheumatoid arthritis; screening the
CC efficacy of a candidate drug in vitro for the treatment of collagen-
CC induced arthritis; and reducing the symptoms associated with collagen-
CC induced arthritis. The compositions of the invention have the following
CC activities: immunosuppressive, antirheumatic, antiarthritic, osteopathic,
CC antigout, antiinflammatory, dermatological, and immunomodulatory. The
CC methods and compositions of the present invention are useful for
CC diagnosing and treating autoimmune disease or arthritides, such as
CC rheumatoid arthritis, lupus, ankylosing spondylitis, fibrositis,
CC fibromyalgia, osteoarthritis, gout, juvenile rheumatoid arthritis, and an
CC immune disease caused by an infectious agent. This polynucleotide
CC represents a DNA sequence relating to the genes used in the analysis and
CC treatment of autoimmune diseases or arthritides. Note: This sequence is
CC not shown in the specification. It has been supplied in an electronic
CC format from WIPO.
XX
SQ Sequence 1505 BP; 438 A; 311 C; 333 G; 423 T; 0 U; 0 Other;

Query Match 99.7%; Score 512.4; DB 11; Length 1505;
Best Local Similarity 99.8%; Pred. No. 7e-129;
Matches 513; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GGACATCTCTTTGGTGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAGATTCAGA 60
DB 972 GGACATCTCTTTGGTGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAGATTCAGA 1031
QY 61 TGTGGTATTGCCCTGGATGATGATGTTTCCACTGGGTGATGAAGTATATTCAGAAAT 120
DB 1032 TGTGGTATTGCCCTGGATGATGATGTTTCCACTGGGTGATGAAGTATATTCAGAAAT 1091
QY 121 CCTCAGCCCTCTTTTATCACTCTGAATATTTCCAAATATCTCTGCTAATATCATATAA 180
DB 1092 CCTCAGCCCTCTTTTATCACTCTGAATATTTCCAAATATCTCTGCTAATATCATATAA 1151
QY 181 ATGAAAAAATGCTACTCACCTGATAAAGAAAGAGATGATTACAATCAGGGGTTCAATC 240
DB 1152 ATGAAAAAATGCTACTCACCTGATAAAGAAAGAGATGATTACAATCAGGGGTTCAATC 1211
QY 241 CACCAGAAATTTGCTGACTTTCACCTTTTGCAACTGGCAAAATAATTGGACACATGCTCAA 300
DB 1212 CACCAGAAATTTGCTGACTTTCACCTTTTGCAACTGGCAAAATAATTGGACACATGCTCAA 1271
QY 301 TTAAGGGACACATAGATTCAATGACGCTATTGATCTTAGCAACAAAGCTTCATTAGCA 360
DB 1272 TTAAGGGACACATAGATTCAATGACGCTATTGATCTTAGCAACAAAGCTTCATTAGCA 1331
QY 361 TTCTTACAAAGCAATTTAGGACTTTCATAAGATTTTGTAGTGGGACTGCTTGAATTGAA 420
DB 1332 TTCTTACAAAGCAATTTAGGACTTTCATAAGATTTTGTAGTGGGACTGCTTGAATTGAA 1391
QY 421 GGAGATGATGAGAAATCTTATTCCAGGGACCAACATTAAACAAACCAATCAACACATCATG 480
DB 1392 GGAGATGATGAGAAATCTTATTCCAGGGACCAACATTAAACAAACCAATCAACACATCATG 1451
QY 481 TTACAGAACTCTTCAGGAATAGAGAATACAATT 514
DB 1452 TTACAGAACTCTTCAGGAATAGAGAATACAATT 1485

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OM nucleic - nucleic search, using sw model

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Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

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Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/1/ina/backfiles.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	514	100.0	1361	2	US-08-557-892-9
2	514	100.0	1361	2	US-08-387-858A-9
3	514	100.0	1361	3	US-09-294-384B-9
4	514	100.0	1361	3	US-08-717-079-9
5	512.4	99.7	1335	1	US-08-483-232-30
6	512.4	99.7	1335	2	US-08-485-938A-30
7	512.4	99.7	1335	2	US-08-910-041-30
8	512.4	99.7	1335	3	US-09-328-474-30
9	512.4	99.7	1335	3	US-09-100-546-30
10	512.4	99.7	1335	3	US-09-010-715-30
11	512.4	99.7	1335	3	US-09-577-758-30
12	512.4	99.7	1520	1	US-08-470-187-7
13	512.4	99.7	1520	1	US-08-318-905-7
14	512.4	99.7	1520	1	US-08-483-232-7
15	512.4	99.7	1520	1	US-08-483-140-7
16	512.4	99.7	1520	2	US-08-485-938A-7
17	512.4	99.7	1520	2	US-08-910-041-7
18	512.4	99.7	1520	3	US-09-328-474-7
19	512.4	99.7	1520	3	US-09-100-546-7
20	512.4	99.7	1520	3	US-09-010-715-7
21	512.4	99.7	1520	3	US-09-577-758-7
22	509.2	99.1	572	2	US-08-557-892-8
23	509.2	99.1	572	2	US-08-387-858A-8
24	509.2	99.1	572	2	US-09-294-384B-8
25	509.2	99.1	572	3	US-08-717-079-8
26	403.6	78.5	2191	1	US-08-318-905-22
27	403.6	78.5	2191	1	US-08-483-232-22

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29	403.6	78.5	2191	2	US-08-485-938A-22	Sequence 22, Appl
30	403.6	78.5	2191	2	US-08-910-041-22	Sequence 22, Appl
31	403.6	78.5	2191	3	US-09-328-474-22	Sequence 22, Appl
32	403.6	78.5	2191	3	US-09-100-546-22	Sequence 22, Appl
33	403.6	78.5	2191	3	US-09-010-715-22	Sequence 22, Appl
34	403.6	78.5	2191	3	US-08-577-758-22	Sequence 22, Appl
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36	402	78.2	1533	2	US-08-485-938A-23	Sequence 23, Appl
37	402	78.2	1533	2	US-08-910-041-23	Sequence 23, Appl
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39	402	78.2	1533	3	US-09-100-546-23	Sequence 23, Appl
40	402	78.2	1533	3	US-09-010-715-23	Sequence 23, Appl
41	402	78.2	1533	3	US-08-577-758-23	Sequence 23, Appl
C 42	390.2	75.9	420	2	US-08-557-892-5	Sequence 5, Appl
C 43	390.2	75.9	420	2	US-08-387-858A-5	Sequence 5, Appl
C 44	390.2	75.9	420	3	US-09-294-384B-5	Sequence 5, Appl
C 45	390.2	75.9	420	3	US-08-717-079-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-08-557-892-9
; Sequence 9, Application US/08557892
; Patent No. 5968818
; GENERAL INFORMATION:
; APPLICANT: MacPhee, Colin Houston
; APPLICANT: Tew, David Graham
; APPLICANT: Southan, Christopher Donald
; APPLICANT: Hickey, Dierdre Mary Bernadette
; APPLICANT: Gloger, Israel Simon
; APPLICANT: Lawrence, Geoffrey Mark Prouse
; APPLICANT: Rice, Simon Quentyn John
; TITLE OF INVENTION: Compounds
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Smithline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/557,892
; FILING DATE: 14 No. 5968818ember 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/387,858
; FILING DATE: 14 No. 5968818ember 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dustman, Wayne J.
; REGISTRATION NUMBER: 33,870
; REFERENCE/DOCKET NUMBER: P30693C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5023
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1361 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO

GENERAL INFORMATION:
APPLICANT: MacPhee, Colin Houston
APPLICANT: Tew, David Graham
APPLICANT: Southan, Christopher Donald
APPLICANT: Hickey, Dierdre Mary Bernadette
APPLICANT: Gloger, Israel Simon
APPLICANT: Lawrence, Geoffrey Mark Prouse
APPLICANT: Rice, Simon Quentyn John
TITLE OF INVENTION: Compounds
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/294,384B
FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/08/387,858
FILING DATE: 24 February 1995
APPLICATION NUMBER: PCT/GB94/01374
FILING DATE: 24 June 1994
ATTORNEY/AGENT INFORMATION:
NAME: Dustman, Wayne J.
REGISTRATION NUMBER: 33,870
REFERENCE/DOCKET NUMBER: P30693
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5023
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1361 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cdna
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 38..1360
US-09-294-384B-9
Query Match 100.0%; Score 514; DB 3; Length 1361;
Best Local Similarity 100.0%; Pred. No. 1.1e-143; Indels 0; Gaps 0;
Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGCAATCTTTTGGTGGGCAACGGTTATTCCAGACTCTTAGTGAAGATCAGAGATTGAGA 60
Db 848 GGCAATCTTTTGGTGGGCAACGGTTATTCCAGACTCTTAGTGAAGATCAGAGATTGAGA 907
Qy 61 TGTGGTATGTCCTGGATGATGATGTTTCCACTGGGTGATGAAGTATATTCAGAAATT 120
Db 908 TGTGGTATGTCCTGGATGATGATGTTTCCACTGGGTGATGAAGTATATTCAGAAATT 967
Qy 121 CCTCAGCCCTCTTTTATCACTCACTCAATTTCCAAATCTCTGCTATATCATATAAA 180
Db 968 CCTCAGCCCTCTTTTATCACTCACTCAATTTCCAAATCTCTGCTATATCATATAAA 1027
Qy 181 ATGAAAAATGCTACTCACCTGATAAAGAAAGAGATGATTACAATCAGGGGTTGAGTC 240
Db 1028 ATGAAAAATGCTACTCACCTGATAAAGAAAGAGATGATTACAATCAGGGGTTGAGTC 1087

241 CACGAGAAATTTTGTGCTGACTTCACTTTTGGCAACTGGCAAAATTAATTGGACACATGCTCAA 300
1088 CACGAGAAATTTTGTGCTGACTTCACTTTTGGCAACTGGCAAAATTAATTGGACACATGCTCAA 1147
301 TTAAGGGAGACATAGATTCAAAATGCAGCTATTGATCTTAGCAACAAAGCTTCAATTAGCA 360
1148 TTAAGGGAGACATAGATTCAAAATGCAGCTATTGATCTTAGCAACAAAGCTTCAATTAGCA 1207
361 TTCTTACAAAAGCATTTAGGACTTCAAAAGATTTTGTATCAGTGGGACTGCTTCAATTGAA 420
1208 TTCTTACAAAAGCATTTAGGACTTCAAAAGATTTTGTATCAGTGGGACTGCTTCAATTGAA 1267
421 GGAGATGATGAGAAATCTTATTCCAGGGAGCAACATTAAACAACAACCAATCAACACATCATG 480
1268 GGAGATGATGAGAAATCTTATTCCAGGGAGCAACATTAAACAACAACCAATCAACACATCATG 1327
481 TTACAGAACTCTTTCAGGAATAGAGAAATACAAAT 514
1328 TTACAGAACTCTTTCAGGAATAGAGAAATACAAAT 1361

RESULT 4
US-08-717-079-9
Sequence 9, Application US/08717079
Patent No. 6369045
GENERAL INFORMATION:
APPLICANT: MacPhee, Colin Houston
APPLICANT: Tew, David Graham
APPLICANT: Southan, Christopher Donald
APPLICANT: Hickey, Dierdre Mary Bernadette
APPLICANT: Gloger, Israel Simon
APPLICANT: Lawrence, Geoffrey Mark Prouse
APPLICANT: Rice, Simon Quentyn John
TITLE OF INVENTION: Compounds
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/717,079
FILING DATE:
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/387,858
FILING DATE: 24 February 1995
APPLICATION NUMBER: PCT/GB94/01374
FILING DATE: 24 June 1994
ATTORNEY/AGENT INFORMATION:
NAME: Dustman, Wayne J.
REGISTRATION NUMBER: 33,870
REFERENCE/DOCKET NUMBER: P30693
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5023
TELEFAX: 610-270-5090
TELEX:
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1361 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cdna
HYPOTHETICAL: NO
ANTI-SENSE: NO

FEATURE:
NAME/KEY: CDS
LOCATION: 38..1360
US-08-717-079-9

Query Match 100.0%; Score 514; DB 3; Length 1361;
Best Local Similarity 100.0%; Pred. No. 1.1e-143;
Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGCAATCTTTTGGTGAGCAACGGTATTTCAGACTCTTAGTGAAGATCAGAGATTGAGA 60
DB 848 GGCAATCTTTTGGTGAGCAACGGTATTTCAGACTCTTAGTGAAGATCAGAGATTGAGA 907
QY 61 TGTGGTATGCGCTGGATGATGATTTCCACTGGGTGATGAAGTATATTCAGAAATT 120
DB 908 TGTGGTATGCGCTGGATGATGATTTCCACTGGGTGATGAAGTATATTCAGAAATT 967
QY 121 CCTCAGCCCTCTTTTATCACTCTGAATATTTCCAAATATCTGCTAATATCATATAA 180
DB 968 CCTCAGCCCTCTTTTATCACTCTGAATATTTCCAAATATCTGCTAATATCATATAA 1027
QY 181 ATGAAAAATGCTACTCACCTGATAAAGAAAGAGATGATTACAATCAGGGTTCAGTC 240
DB 1028 ATGAAAAATGCTACTCACCTGATAAAGAAAGAGATGATTACAATCAGGGTTCAGTC 1087
QY 241 CACGAGAAATTTGCTGACTTCACTTTTGCACCTGGCAAAATAATTGGACACATGCTCAAA 300
DB 1088 CACGAGAAATTTGCTGACTTCACTTTTGCACCTGGCAAAATAATTGGACACATGCTCAAA 1147
QY 301 TTAAGGGAGACATAGATCAATGACCTATTGATCTTAGCAACAAGCTTCATTAGCA 360
DB 1148 TTAAGGGAGACATAGATCAATGACCTATTGATCTTAGCAACAAGCTTCATTAGCA 1207
QY 361 TTCTTACAAAAGCAATTTAGACTTCATAAAGATTTTGCATGAGGGAGCTCTTGAATTGAA 420
DB 1208 TTCTTACAAAAGCAATTTAGACTTCATAAAGATTTTGCATGAGGGAGCTCTTGAATTGAA 1267
QY 421 GGAGATGATGAGATCTTTATTCAGGGACCAACATTAACCAACCAATCAACACATCATG 480
DB 1268 GGAGATGATGAGATCTTTATTCAGGGACCAACATTAACCAACCAATCAACACATCATG 1327
QY 481 TTACAGAACTCTTCAGGAATAGAAATACAATT 514
DB 1328 TTACAGAACTCTTCAGGAATAGAAATACAATT 1361

RESULT 5

US-08-483-232-30
Sequence 30, Application US/08483232
Patent No. 5656431
GENERAL INFORMATION:
APPLICANT: Cousins, Lawrence S.
APPLICANT: Eberhardt, Christine D.
APPLICANT: Gray, Patrick W.
APPLICANT: Le Trong, Hai
APPLICANT: Tjoelker, Larry W.
APPLICANT: Wilder, Cheryl L.
TITLE OF INVENTION: Platelet-Activating Factor
TITLE OF INVENTION: Acetylhydrolase
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/483,232
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/318,905
FILING DATE: 06-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,803
FILING DATE: 06-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: No. 565643land, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/32689
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3658
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 1335 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
US-08-483-232-30

Query Match 99.7%; Score 512.4; DB 1; Length 1335;

Best Local Similarity 99.8%; Pred. No. 3.2e-143;

Matches 513; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGCAATCTTTTGGTGAGCAACGGTATTTCAGACTCTTAGTGAAGATCAGAGATTGAGA 60
DB 811 GGCAATCTTTTGGTGAGCAACGGTATTTCAGACTCTTAGTGAAGATCAGAGATTGAGA 870
QY 61 TGTGGTATGCGCTGGATGATGATTTCCACTGGGTGATGAAGTATATTCAGAAATT 120
DB 871 TGTGGTATGCGCTGGATGATGATTTCCACTGGGTGATGAAGTATATTCAGAAATT 930
QY 121 CCTCAGCCCTCTTTTATCACTCTGAATATTTCCAAATATCTGCTAATATCATATAA 180
DB 931 CCTCAGCCCTCTTTTATCACTCTGAATATTTCCAAATATCTGCTAATATCATATAA 990
QY 181 ATGAAAAATGCTACTCACCTGATAAAGAAAGAGATGATTACAATCAGGGTTCAGTC 240
DB 991 ATGAAAAATGCTACTCACCTGATAAAGAAAGAGATGATTACAATCAGGGTTCAGTC 1050
QY 241 CACGAGAAATTTGCTGACTTCACTTTTGCACCTGGCAAAATAATTGGACACATGCTCAAA 300
DB 1051 CACGAGAAATTTGCTGACTTCACTTTTGCACCTGGCAAAATAATTGGACACATGCTCAAA 1110
QY 301 TTAAGGGAGACATAGATCAATGACCTATTGATCTTAGCAACAAGCTTCATTAGCA 360
DB 1111 TTAAGGGAGACATAGATCAATGACCTATTGATCTTAGCAACAAGCTTCATTAGCA 1170
QY 361 TTCTTACAAAAGCAATTTAGACTTCATAAAGATTTTGCATGAGGGAGCTCTTGAATTGAA 420
DB 1171 TTCTTACAAAAGCAATTTAGACTTCATAAAGATTTTGCATGAGGGAGCTCTTGAATTGAA 1230
QY 421 GGAGATGATGAGATCTTTATTCAGGGACCAACATTAACCAACCAATCAACACATCATG 480
DB 1231 GGAGATGATGAGATCTTTATTCAGGGACCAACATTAACCAACCAATCAACACATCATG 1290
QY 481 TTACAGAACTCTTCAGGAATAGAAATACAATT 514
DB 1291 TTACAGAACTCTTCAGGAATAGAAATACAATT 1324

RESULT 6

US-08-485-938A-30
Sequence 30, Application US/08485938A
Patent No. 5847088
GENERAL INFORMATION:
APPLICANT: Cousins, Lawrence S.

APPLICANT: Eberhardt, Christine D.
APPLICANT: Gray, Patrick W.
APPLICANT: Le Trong, Hai
APPLICANT: Tjoelker, Larry W.
APPLICANT: Wilder, Cheryl L.
TITLE OF INVENTION: Platelet-Activating Factor
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/485,938A
FILING DATE: 06-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 08/318,905
FILING DATE: 06-OCT-1994
PRIOR APPLICATION NUMBER: US 08/133,803
FILING DATE: 06-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: No. 5847088and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/32792
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3658
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 1335 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-485-938A-30

Query Match 99.7%; Score 512.4; DB 2; Length 1335;
Best Local Similarity 99.8%; Pred. No. 3.2e-143;
Matches 513; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGACATTCCTTTGGTGGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAGATTGAGA 60
Db 811 GGACATTCCTTTGGTGGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAGATTGAGA 870

Qy 61 TGTGGTATGCGCTGGATGATGATGTTCCACTGGGTGATGAAGTATATTCAGAAATT 120
Db 871 TGTGGTATGCGCTGGATGATGATGTTCCACTGGGTGATGAAGTATATTCAGAAATT 930

Qy 121 CCTCAGCCCTCTTTTATCACTGCAATATTTCCAAATATCTGCTATATCATATAA 180
Db 931 CCTCAGCCCTCTTTTATCACTGCAATATTTCCAAATATCTGCTATATCATATAA 990

Qy 181 ATGAAAAAATCTACTCCTGATGATAAGAAAGAGATGATTACAACTCAGGGTTCAGTC 240
Db 991 ATGAAAAAATGCTACTCCTGATGATAAGAAAGAGATGATTACAACTCAGGGTTCAGTC 1050

Qy 241 CACCAGAAATTTGCTGACTTCACCTTTTGCATCGCAAAATTAATGGACATGCTCAAA 300
Db 1051 CACCAGAAATTTGCTGACTTCACCTTTTGCATCGCAAAATTAATGGACATGCTCAAA 1110

Qy 301 TTAAGGAGACATAGATTCAATTCAGCTATTGATCTTAGCAACAAAGCTTCATTAGCA 360
Db 1111 TTAAGGAGACATAGATTCAATTCAGCTATTGATCTTAGCAACAAAGCTTCATTAGCA 1170

Qy 361 TTCTTACAAAAGCATTTAGGACTTCATAAAGATTTTGTATCAGTGGGACTGCTTGAATTGAA 420
Db 1171 TTCTTACAAAAGCATTTAGGACTTCATAAAGATTTTGTATCAGTGGGACTGCTTGAATTGAA 1230

Qy 421 GGAGATGATGAGATCTTTATTCAGGGAGCAACCAATTAACCAACCAATCAACATCATG 480
Db 1231 GGAGATGATGAGATCTTTATTCAGGGAGCAACCAATTAACCAACCAATCAACATCATG 1290

Qy 481 TTACAGAACTCTTCAGGAATAGAGAAATACAAAT 514
Db 1291 TTACAGAACTCTTCAGGAATAGAGAAATACAAAT 1324

RESULT 7
US-08-910-041-30
Sequence 30, Application US/08910041
Patent No. 5977308
GENERAL INFORMATION:
APPLICANT: Cousens, Lawrence S.
APPLICANT: Eberhardt, Christine D.
APPLICANT: Gray, Patrick W.
APPLICANT: Le Trong, Hai
APPLICANT: Tjoelker, Larry W.
APPLICANT: Wilder, Cheryl L.
TITLE OF INVENTION: Platelet-Activating Factor
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/910,041
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/483,232
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/318,905
FILING DATE: 06-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,803
FILING DATE: 06-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Rin-Laures, Li-Hsien
REGISTRATION NUMBER: 33,547
REFERENCE/DOCKET NUMBER: 27866/34026
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3658
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 1335 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-910-041-30

Query Match 99.7%; Score 512.4; DB 2; Length 1335;
Best Local Similarity 99.8%; Pred. No. 3.2e-143;
Matches 513; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Matches 513; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGACATCTTTTGGTGGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAGATTTCAGA 60
DB 811 GGACATCTTTTGGTGGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAGATTTCAGA 870

QY 61 TGTGGTATTCCTTGGTGGATGATGATGTTTCCACTGGGTGATGAAGTATATTCAGAAAT 120
DB 871 TGTGGTATTCCTTGGTGGATGATGATGTTTCCACTGGGTGATGAAGTATATTCAGAAAT 930

QY 121 CCTCAGCCCTCTTTTATCACTCTGAATATTTCCAAATATCTGCTTAATATCATATAA 180
DB 931 CCTCAGCCCTCTTTTATCACTCTGAATATTTCCAAATATCTGCTTAATATCATATAA 990

QY 181 ATGAAAAATGCTACTCCTGATGATAAAGAAAGAGATGATTACAATCAGGGGTTTCAGTC 240
DB 991 ATGAAAAATGCTACTCCTGATGATAAAGAAAGAGATGATTACAATCAGGGGTTTCAGTC 1050

QY 241 CACCAGAAATTTGCTGACTTCACTTTTGGCACTGGCAAAATAATTTGGACACATGCTCAAA 300
DB 1051 CACCAGAAATTTGCTGACTTCACTTTTGGCACTGGCAAAATAATTTGGACACATGCTCAAA 1110

QY 301 TTAAGGGGACATAGATTCATATGACCTTATTAAGATTTTTCAGTGGGACTGCTTGAATGAA 360
DB 1111 TTAAGGGGACATAGATTCATATGACCTTATTAAGATTTTTCAGTGGGACTGCTTGAATGAA 1170

QY 421 GGAGATGATGAGATCTTATTCAGGGACCAACATTAACCAACCAATCAACACATCATG 480
DB 1231 GGAGATGATGAGATCTTATTCAGGGACCAACATTAACCAACCAATCAACACATCATG 1290

QY 481 TTACAGAACTCTTCAGGAATAGAGAAATACAATT 514
DB 1291 TTACAGAACTCTTCAGGAATAGAGAAATACAATT 1324

RESULT 8
US-09-328-474-30
; Sequence 30, Application US/09328474
; Patent No. 6045794
; GENERAL INFORMATION:
; APPLICANT: Cousins, Lawrence S.
; APPLICANT: Eberhardt, Christine D.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Le Trong, Hai
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor
; TITLE OF INVENTION: Acetylhydrolase
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/328,474
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/483,232
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/318,905
; FILING DATE: 06-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 06-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Rin-Laures, Li-Hsien
; REGISTRATION NUMBER: 33,547
; REFERENCE/DOCKET NUMBER: 27866/34026
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3658
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1335 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-09-328-474-30

Query Match 99.7%; Score 512.4; DB 3; Length 1335;
Best Local Similarity 99.8%; Pred. No. 3.2e-143;
Matches 513; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGACATCTTTTGGTGGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAGATTTCAGA 60
DB 811 GGACATCTTTTGGTGGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAGATTTCAGA 870

QY 61 TGTGGTATTCCTTGGTGGATGATGATGTTTCCACTGGGTGATGAAGTATATTCAGAAAT 120
DB 871 TGTGGTATTCCTTGGTGGATGATGATGTTTCCACTGGGTGATGAAGTATATTCAGAAAT 930

QY 121 CCTCAGCCCTCTTTTATCACTCTGAATATTTCCAAATATCTGCTTAATATCATATAA 180
DB 931 CCTCAGCCCTCTTTTATCACTCTGAATATTTCCAAATATCTGCTTAATATCATATAA 990

QY 181 ATGAAAAATGCTACTCCTGATGATAAAGAAAGAGATGATTACAATCAGGGGTTTCAGTC 240
DB 991 ATGAAAAATGCTACTCCTGATGATAAAGAAAGAGATGATTACAATCAGGGGTTTCAGTC 1050

QY 241 CACCAGAAATTTGCTGACTTCACTTTTGGCACTGGCAAAATAATTTGGACACATGCTCAAA 300
DB 1051 CACCAGAAATTTGCTGACTTCACTTTTGGCACTGGCAAAATAATTTGGACACATGCTCAAA 1110

QY 301 TTAAGGGGACATAGATTCATATGACCTTATTAAGATTTTTCAGTGGGACTGCTTGAATGAA 360
DB 1111 TTAAGGGGACATAGATTCATATGACCTTATTAAGATTTTTCAGTGGGACTGCTTGAATGAA 1170

QY 421 GGAGATGATGAGATCTTATTCAGGGACCAACATTAACCAACCAATCAACACATCATG 480
DB 1231 GGAGATGATGAGATCTTATTCAGGGACCAACATTAACCAACCAATCAACACATCATG 1290

QY 481 TTACAGAACTCTTCAGGAATAGAGAAATACAATT 514
DB 1291 TTACAGAACTCTTCAGGAATAGAGAAATACAATT 1324

RESULT 9
US-09-100-546-30
; Sequence 30, Application US/09100546
; Patent No. 6099836
; GENERAL INFORMATION:
; APPLICANT: Cousins, Lawrence S.
; APPLICANT: Eberhardt, Christine D.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Le Trong, Hai
; APPLICANT: Tjoelker, Larry W.

```
;; APPLICANT: Wilder, Cheryl L.
;; TITLE OF INVENTION: Platelet-Activating Factor
;; TITLE OF INVENTION: Acetylhydrolase
;; NUMBER OF SEQUENCES: 30
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
;; STREET: 6300 Sears Tower, 233 South Wacker Drive
;; CITY: Chicago
;; STATE: Illinois
;; COUNTRY: United States of America
;; ZIP: 60606-6402
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/100,546
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/09/010,715
;; FILING DATE:
;; APPLICATION NUMBER: US 08/318,905
;; FILING DATE: 06-OCT-1993
;; TITLE OF INVENTION: Platelet-Activating Factor
;; TITLE OF INVENTION: Acetylhydrolase
;; NUMBER OF SEQUENCES: 30
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
;; STREET: 6300 Sears Tower, 233 South Wacker Drive
;; CITY: Chicago
;; STATE: Illinois
;; COUNTRY: United States of America
;; ZIP: 60606-6402
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/010,715
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/318,905
;; FILING DATE: 06-OCT-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/133,803
;; FILING DATE: 06-OCT-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: No. 6099836and, Greta E.
;; REGISTRATION NUMBER: 35,302
;; REFERENCE/DOCKET NUMBER: 27866/32793
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (312) 474-6300
;; TELEFAX: (312) 474-0448
;; TELEX: 25-3658
;; INFORMATION FOR SEQ ID NO: 30:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1335 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cdna
;; US-09-100-546-30

Query Match          99.7%; Score 512.4; DB 3; Length 1335;
Best Local Similarity 99.8%; Pred. No. 3.2e-143;
Matches 513; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1  GGACATCTTTTGGTGAGCAACGGTTATTTCAGACTCTTTAGTGAAGATTCAGAGATTTCAGA 60
Db      811 GGACATCTTTTGGTGAGCAACGGTTATTTCAGACTCTTTAGTGAAGATTCAGAGATTTCAGA 870

Qy      61  TGTGGTATGCGCTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120
Db      871 TGTGGTATGCGCTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 930

Qy      121 CCTCAGCCCTCTTTTATCAACTCTGAATATTTCAATATCTCTGCTAATATCATATAAA 180
Db      931 CCTCAGCCCTCTTTTATCAACTCTGAATATTTCAATATCTCTGCTAATATCATATAAA 990

Qy      181 ATGAAAAAATGCTACTCACTGATAAAGAAAGAAAGATGATTAACAATCAGGGGTTTCAGTC 240
Db      991 ATGAAAAAATGCTACTCACTGATAAAGAAAGAAAGATGATTAACAATCAGGGGTTTCAGTC 1050

Qy      241 CACCAGATTTTGTGCTGCTTCACTTTCACCTGGCACTGGCACTGGCACTGGCACTGGCACTGGCA 300
Db      1051 CACCAGATTTTGTGCTGCTTTCACCTGGCACTGGCACTGGCACTGGCACTGGCACTGGCA 1110

Qy      301 TTAAGGGAGACATAGATTCAAATGACGACTATTGATCTTTAGCAACAAGCTTCATTAGCA 360
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Qy      361 TTCTTACAAAAGCATTTAGGACTTCATAAAGATTTTTCAGTGGGACTGCTTCAATTCAA 420
Db      1171 TTCTTACAAAAGCATTTAGGACTTCATAAAGATTTTTCAGTGGGACTGCTTCAATTCAA 1230

Qy      421 GGAGATGATGAGATCTTATTTCAGGGAGCAACCAATTAACAACAACAATCAACATCATG 480
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RESULT 10
US-09-010-715-30
; Sequence 30, Application US/09010715
; Patent No. 6146625
; GENERAL INFORMATION:
; APPLICANT: Cousens, Lawrence S.
; APPLICANT: Eberhardt, Christine D.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Le Trong, Hai
; APPLICANT: Tjoelker, Larry L.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor
; TITLE OF INVENTION: Acetylhydrolase
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,715
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/318,905
; FILING DATE: 06-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 06-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6146625and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/32793
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3658
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1335 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; US-09-010-715-30

Query Match          99.7%; Score 512.4; DB 3; Length 1335;
Best Local Similarity 99.8%; Pred. No. 3.2e-143;
Matches 513; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      61  TGTGGTATGCGCTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120
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Qy      121 CCTCAGCCCTCTTTTATCAACTCTGAATATTTCAATATCTCTGCTAATATCATATAAA 180
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Qy      241 CACCAGATTTTGTGCTGCTTCACTTTCACCTGGCACTGGCACTGGCACTGGCACTGGCACTGGCA 300
Db      1051 CACCAGATTTTGTGCTGCTTTCACCTGGCACTGGCACTGGCACTGGCACTGGCACTGGCA 1110

Qy      301 TTAAGGGAGACATAGATTCAAATGACGACTATTGATCTTTAGCAACAAGCTTCATTAGCA 360
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COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/470,187
FILING DATE:
PRIORITY APPLICATION DATA:
CLASSIFICATION: 435
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: No. 5532152and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31672
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3658
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1520 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
FEATURE:
NAME/KEY: CDS
LOCATION: 162..1484
US-08-470-187-7

Query Match 99.7%; Score 512.4; DB 1; Length 1520;
Best Local Similarity 99.8%; Pred. No. 3.4e-143;
Matches 513; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GGACATTCCTTTGGTGGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAGATTTCAGA 60
Db 972 GGACATTCCTTTGGTGGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAGATTTCAGA 1031
Qy 61 TGTGGTATTCCTCGGATGCATGATGTTCCACTGGGTGATGAAGTATATTCAGAAATT 120
Db 1032 TGTGGTATTCCTCGGATGCATGATGTTCCACTGGGTGATGAAGTATATTCAGAAATT 1091
Qy 121 CCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAATATCTGCTTAATATCATATAA 180
Db 1092 CCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAATATCTGCTTAATATCATATAA 1151
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Db 1152 ATGAAAAATGCTACTCACCTGATAAAGAAAGAGATGATTACAATCAGGGGTTTCAGTC 1211
Qy 241 CACGAGATTTTGTGACTTCACCTTTGCAACTGGCAAAATTAATGGACATGCTCAAA 300
Db 1212 CACGAGATTTTGTGACTTCACCTTTGCAACTGGCAAAATTAATGGACATGCTCAAA 1271
Qy 301 TTAAGGAGACATAGATTCAAAATGCAGCTATTGATCTTAGCAACAAAGCTTCATTAGCA 360
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Db 1332 TTCTTACAAAAGCATTTAGGACTTCATAAAGATTTTGAATCAGTGGGACTGCTGATTGAA 1391
Qy 421 GGAGATGATGAGATCTTTATTTCCAGGGACCAACATTAACACAAACAATCAACATCATG 480
Db 1392 GGAGATGATGAGATCTTTATTTCCAGGGACCAACATTAACACAAACAATCAACATCATG 1451
Qy 481 TTACAGAACTCTTCAGGATAGAGAAATACAAATT 514
Db 1452 TTACAGAACTCTTCAGGATAGAGAAATACAAATT 1485

RESULT 13
US-08-318-905-7
Sequence 7, Application US/08318905
Patent No. 5641669
GENERAL INFORMATION:
APPLICANT: Cousens, Lawrence S.
APPLICANT: Eberhardt, Christine D.
APPLICANT: Gray, Patrick W.
APPLICANT: Le Trong, Hai
APPLICANT: Tjoelker, Larry W.
APPLICANT: Wilder, Cheryl L.
TITLE OF INVENTION: Platelet-Activating Factor Acetyl
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gertein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/318,905
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,803
FILING DATE: 6-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: No. 5641669and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 32205
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3658
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1520 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
FEATURE:
NAME/KEY: CDS
LOCATION: 162..1484
US-08-318-905-7

Query Match 99.7%; Score 512.4; DB 1; Length 1520;
Best Local Similarity 99.8%; Pred. No. 3.4e-143;
Matches 513; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GGACATTCCTTTGGTGGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAGATTTCAGA 60
Db 972 GGACATTCCTTTGGTGGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAGATTTCAGA 1031
Qy 61 TGTGGTATTCCTCGGATGCATGATGTTCCACTGGGTGATGAAGTATATTCAGAAATT 120
Db 1032 TGTGGTATTCCTCGGATGCATGATGTTCCACTGGGTGATGAAGTATATTCAGAAATT 1091
Qy 121 CCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAATATCTGCTTAATATCATATAA 180
Db 1092 CCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAATATCTGCTTAATATCATATAA 1151
Qy 181 ATGAAAAATGCTACTCACCTGATAAAGAAAGATGATTACAATCAGGGGTTTCAGTC 240

Db 1152 ATGAAAAATCTACTCCTGATATAAGAAAGAAAGATGATTACAAATCAGGGGTTCAATC 1211
Qy 241 CACCAGAAATTTGCTGACTTCACTTTTGCACACTGGCAAAATAATTTGGACACATGCTCAAA 300
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Qy 301 TTAAGGGAGACATAGATTCAAAATGCAGCTATTGATCTTTAGCAACAAAGCTTCAATTAGCA 360
Db 1272 TTAAGGGAGACATAGATTCAAAATGCAGCTATTGATCTTTAGCAACAAAGCTTCAATTAGCA 1331
Qy 361 TTCTTACAAAGCAATTTAGGACTTTCATTAAGATTTTTCATGCTGGGACTGCTGATTGAA 420
Db 1332 TTCTTACAAAGCAATTTAGGACTTTCATTAAGATTTTTCATGCTGGGACTGCTGATTGAA 1391
Qy 421 GGAGATGATGAGATCTTTATTCAGGACCAACAAATTAACCAACCAATTAACCAACATCATG 480
Db 1392 GGAGATGATGAGATCTTTATTCAGGACCAACAAATTAACCAACCAATTAACCAACATCATG 1451
Qy 481 TTACAGAACTCTTCAGGAATAGAGAAATACAATT 514
Db 1452 TTACAGAACTCTTCAGGAATAGAGAAATACAATT 1485

RESULT 14

US-08-483-232-7
; Sequence 7, Application US/08483232
; Patent No. 5656431
; GENERAL INFORMATION:
; APPLICANT: Cousens, Lawrence S.
; APPLICANT: Eberhardt, Christine D.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Le Trong, Hai
; APPLICANT: Tjoelker, Larry L.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor
; TITLE OF INVENTION: Acetylhydrolase
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,232
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/318,905
; FILING DATE: 06-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 06-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 565643land, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/32689
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3658
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1520 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 162..1484
US-08-483-232-7

Query Match 99.7%; Score 512.4; DB 1; Length 1520;
Best Local Similarity 99.8%; Pred. No. 3.4e-143;
Matches 513; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGACATCTTTTGGTGAGCAACGGTTTATTTCAGACTCTTTAGTGAAGATCAGAGATTGAGA 60
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Qy 121 CCTCAGCCCTCTTTTTCCTCAACTCTGAAATATTTTCAATATCTCTGCTAATATCATAAAA 180
Db 1092 CCTCAGCCCTCTTTTTCCTCAACTCTGAAATATTTTCAATATCTCTGCTAATATCATAAAA 1151
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Db 1332 TTCTTACAAAGCAATTTAGGACTTTCATTAAGATTTTTCATGCTGGGACTGCTGATTGAA 1391
Qy 421 GGAGATGATGAGATCTTTATTCAGGACCAACCAATTAACCAACCAATTAACCAACATCATG 480
Db 1392 GGAGATGATGAGATCTTTATTCAGGACCAACCAATTAACCAACCAATTAACCAACATCATG 1451
Qy 481 TTACAGAACTCTTCAGGAATAGAGAAATACAATT 514
Db 1452 TTACAGAACTCTTCAGGAATAGAGAAATACAATT 1485

RESULT 15

US-08-483-140-7
; Sequence 7, Application US/08483140
; Patent No. 5698403
; GENERAL INFORMATION:
; APPLICANT: ICOS Corporation
; TITLE OF INVENTION: Platelet-Activating Factor Acetyl
; TITLE OF INVENTION: Hydrolase
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,140
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: US 08/318,905
; FILING DATE: 6-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 6-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5698403and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 32781
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3658
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1520 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 162..1484
; US-08-483-140-7

Query Match      99.7%; Score 512.4; DB 1; Length 1520;
Best Local Similarity 99.8%; Pred. No. 3.4e-143;
Matches 513; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db      972  GGACATTCCTTTTGGTGAGCAACGGTTATTCAGACTCTTAGTGAAGATCAGAGATTTCAGA 1031

Qy      61  TGTGATATTCCTCGATGCATGGATGTTTCCACTGGGTGATGAAGTATATTCAGAAATT 120
Db     1032  TGTGATATTCCTCGATGCATGGATGTTTCCACTGGGTGATGAAGTATATTCAGAAATT 1091

Qy     121  CCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAAATATCTCTGCTAATATCATATAAA 180
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Qy     181  ATGAAAAAATGCTACTCACCTGATAAAGAAAGAGATGATTACAATCAGGGTTTCAGTC 240
Db     1152  ATGAAAAAATGCTACTCACCTGATAAAGAAAGAGATGATTACAATCAGGGTTTCAGTC 1211

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Qy     301  TTAAAGGGAGACATAGATTCAAATGCAGCTATTGATCTTAGCAACAAAGCTTCATTAGCA 360
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Db     1332  TTCTTACAAAAGCATTAGGACTTCATAAAGATTTTGATCAGTGGACTGCTTGATTGAA 1391

Qy     421  GGAGATGATGAGAAATCTTATTTCCAGGGACCAACATTAACACAAACCAATCAACATCATG 480
Db     1392  GGAGATGATGAGAAATCTTATTTCCAGGGACCAACATTAACACAAACCAATCAACATCATG 1451

Qy     481  TTACAGAACTCTTCAGGAATAGAGAAATACAAATT 514
Db     1452  TTACAGAACTCTTCAGGAATAGAGAAATACAAATT 1485
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 Copyright (c) 1993 - 2005 Compugen Ltd.
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Title: US-09-922-067F-9_COPY_848_1361
 Perfect score: 514
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Minimum DB seq length: 0

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 16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq.*
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 22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB ID	Description
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2	514	100.0	1361	15	US-10-173-233-9
3	514	100.0	1361	16	US-10-406-156-9
4	514	100.0	1561	9	US-09-962-832-110
5	513.2	99.8	1845	18	US-10-741-601-89
6	513.2	99.8	1845	18	US-10-741-601-90
7	513	99.8	1323	18	US-10-415-682B-1
8	512.4	99.7	1335	9	US-09-729-402-30
9	512.4	99.7	1335	14	US-10-003-978A-30
10	512.4	99.7	1505	17	US-10-172-118-1120
11	512.4	99.7	1505	17	US-10-342-887-1120

SUMMARIES

12	512.4	99.7	1505	18	US-10-755-889-277	Sequence 277, Appl
13	512.4	99.7	1520	9	US-09-729-402-7	Sequence 7, Appli
14	512.4	99.7	1520	14	US-10-003-978A-7	Sequence 7, Appli
15	509.2	99.1	572	9	US-09-922-067-8	Sequence 8, Appli
16	509.2	99.1	572	15	US-10-173-233-8	Sequence 8, Appli
17	509.2	99.1	572	16	US-10-406-156-8	Sequence 8, Appli
18	403.6	78.5	2191	9	US-09-729-402-22	Sequence 22, Appl
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22	399	77.6	477	10	US-09-918-995-24863	Sequence 24863, A
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c 24	390.2	75.9	420	15	US-10-173-233-5	Sequence 5, Appli
c 25	390.2	75.9	420	16	US-10-406-156-5	Sequence 5, Appli
26	307.6	59.8	517	9	US-09-729-402-25	Sequence 25, Appl
27	307.6	59.8	517	14	US-10-003-978A-25	Sequence 25, Appl
28	302.8	58.9	379	9	US-09-922-067-6	Sequence 6, Appli
29	302.8	58.9	379	15	US-10-173-233-6	Sequence 6, Appli
30	302.8	58.9	379	16	US-10-406-156-6	Sequence 6, Appli
31	284.6	55.4	1494	9	US-09-729-402-21	Sequence 21, Appl
32	284.6	55.4	1494	14	US-10-003-978A-21	Sequence 21, Appl
c 33	238.6	46.4	385	9	US-09-962-832-58	Sequence 58, Appl
c 34	238.6	46.4	385	9	US-09-880-107-1974	Sequence 1974, Ap
c 35	238.6	46.4	385	11	US-09-968-007A-185	Sequence 185, App
c 36	234.4	45.6	441	10	US-09-918-995-13782	Sequence 13782, A
37	215.8	42.0	1876	9	US-09-729-402-24	Sequence 24, Appl
38	215.8	42.0	1876	14	US-10-003-978A-24	Sequence 24, Appl
39	200.6	39.0	201	18	US-10-741-601-2009	Sequence 2009, Ap
40	200.6	39.0	201	18	US-10-741-601-2013	Sequence 2013, Ap
41	200.6	39.0	201	18	US-10-741-601-2017	Sequence 2017, Ap
42	200.6	39.0	201	18	US-10-741-601-2022	Sequence 2022, Ap
43	199.4	38.8	279	9	US-09-922-067-7	Sequence 7, Appli
44	199.4	38.8	279	15	US-10-173-233-7	Sequence 7, Appli
45	199.4	38.8	279	16	US-10-406-156-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1

US-09-922-067-9
 ; Sequence 9, Application US/09922067
 ; Patent No. US2002017720A1

GENERAL INFORMATION:

APPLICANT: MacPhee, Colin Houston
 Tew, David Graham
 Southan, Christopher Donald
 Hickey, Dierdre Mary Bernadette
 Gloger, Israel Simon
 Lawrence, Geoffrey Mark Prouse
 Rice, Simon Quantyn John

TITLE OF INVENTION: Lipoprotein Associated Phospholipase A2, Inhibitors
 Thereof And Use Of The Same In Diagnosis And Therapy

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: SmithKline Beecham Corporation
 STREET: 709 Swedeland Road
 CITY: King of Prussia
 STATE: PA
 COUNTRY: USA
 ZIP: 19406

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/922.067
 FILING DATE: 03-Aug-2001
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/193,130
 FILING DATE: 1998-11-17

APPLICATION NUMBER: PCT/GB94/01374
FILING DATE: 24 June 1994
ATTORNEY/AGENT INFORMATION:
NAME: Dustman, Wayne J.
REGISTRATION NUMBER: 33,870
REFERENCE/DOCKET NUMBER: P30693
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5023
TELEFAX: 610-270-5090
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1361 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cdna
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 38..1360
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-922-067-9

Query Match 100.0%; Score 514; DB 9; Length 1361;
Best Local Similarity 100.0%; Pred. No. 1.7e-127;
Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGACATCTTTTGGTGAGCAACGGTTATTACAGACTCTTAGTGAAGATCAGAGATTGAGA 60
DB 848 GGACATCTTTTGGTGAGCAACGGTTATTACAGACTCTTAGTGAAGATCAGAGATTGAGA 907
QY 61 TGTGGTATTCGCCCTGGATGATGATCTTTCCACTGGTGGTATGAAGTATATCCAGAAAT 120
DB 908 TGTGGTATTCGCCCTGGATGATGATCTTTCCACTGGTGGTATGAAGTATATCCAGAAAT 967
QY 121 CCTCAGCCCTCTTTTATCACTCTGAATATTTCCAAATATCTCTCTAATATCATAAAA 180
DB 968 CCTCAGCCCTCTTTTATCACTCTGAATATTTCCAAATATCTCTCTAATATCATAAAA 1027
QY 181 ATGAAAAATGCTACTCAGCTGATGAAGAAAGAGATGATTACATCAGGGTTCAGTC 240
DB 1028 ATGAAAAATGCTACTCAGCTGATGAAGAAAGAGATGATTACATCAGGGTTCAGTC 1087
QY 241 CACCAGAAATTTGCTGACTTTCACCTTTGGCAACTGGCAAAATATTTGGACACATGCTCAA 300
DB 1088 CACCAGAAATTTGCTGACTTTCACCTTTGGCAACTGGCAAAATATTTGGACACATGCTCAA 1147
QY 301 TTAAGGGAGACATAGATTCAAAATGACGTATTGATCTTAGCAACAAAGCTTCATTAGCA 360
DB 1148 TTAAGGGAGACATAGATTCAAAATGACGTATTGATCTTAGCAACAAAGCTTCATTAGCA 1207
QY 361 TTCTTCAAAAGCATTTAGACATTCATAAAGATTTTGGATGAGTGGGAGCTGCTGATGAA 420
DB 1208 TTCTTCAAAAGCATTTAGACATTCATAAAGATTTTGGATGAGTGGGAGCTGCTGATGAA 1267
QY 421 GGAGATGATCAGAAATCTTATTTCCAGGAGCAACATTAACCAACCAATCAACATCATG 480
DB 1268 GGAGATGATCAGAAATCTTATTTCCAGGAGCAACATTAACCAACCAATCAACATCATG 1327
QY 481 TTACAGAACTCTTCAGGAATAGAGAAATACAAT 514
DB 1328 TTACAGAACTCTTCAGGAATAGAGAAATACAAT 1361

RESULT 2
US-10-173-233-9
; Sequence 9, Application US/10173233
; Publication No. US20030148398A1
; GENERAL INFORMATION:
; APPLICANT: MacPhee, Colin Houston
; Tew, David Graham

Southan, Christopher Donald
Hickey, Dierdre Mary Bernadette
Gloger, Israel Simon
Lawrence, Geoffrey Mark Prouse
Rice, Simon Quentyn John
TITLE OF INVENTION: Compounds
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/173,233
FILING DATE: 14-Jun-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/569,899
FILING DATE: 12-May-2000
ATTORNEY/AGENT INFORMATION:
NAME: Dustman, Wayne J.
REGISTRATION NUMBER: 33,870
REFERENCE/DOCKET NUMBER: P30693
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5023
TELEFAX: 610-270-5090
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1361 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cdna
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 38..1360
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-173-233-9

Query Match 100.0%; Score 514; DB 15; Length 1361;
Best Local Similarity 100.0%; Pred. No. 1.7e-127;
Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGACATCTTTTGGTGAGCAACGGTTATTACAGACTCTTAGTGAAGATCAGAGATTGAGA 60
DB 848 GGACATCTTTTGGTGAGCAACGGTTATTACAGACTCTTAGTGAAGATCAGAGATTGAGA 907
QY 61 TGTGGTATTCGCCCTGGATGATGATCTTTCCACTGGTGGTATGAAGTATATCCAGAAAT 120
DB 908 TGTGGTATTCGCCCTGGATGATGATCTTTCCACTGGTGGTATGAAGTATATCCAGAAAT 967
QY 121 CCTCAGCCCTCTTTTATCACTCTGAATATTTCCAAATATCTCTCTAATATCATAAAA 180
DB 968 CCTCAGCCCTCTTTTATCACTCTGAATATTTCCAAATATCTCTCTAATATCATAAAA 1027
QY 181 ATGAAAAATGCTACTCAGCTGATGAAGAAAGAGATGATTACATCAGGGTTCAGTC 240
DB 1028 ATGAAAAATGCTACTCAGCTGATGAAGAAAGAGATGATTACATCAGGGTTCAGTC 1087
QY 241 CACCAGAAATTTGCTGACTTTCACCTTTGGCAACTGGCAAAATATTTGGACACATGCTCAA 300
DB 1088 CACCAGAAATTTGCTGACTTTCACCTTTGGCAACTGGCAAAATATTTGGACACATGCTCAA 1147

QY 301 TTAAAGGAGACATAGATTCAAAATGCAGCTATTGATCTTAGCAACAAGCTTCATTAGCA 360
Db 1148 TTAAAGGAGACATAGATTCAAAATGCAGCTATTGATCTTAGCAACAAGCTTCATTAGCA 1207
QY 361 TTCTTACAAAAGCATTTAGGACTTCATAAAGATTTTATCAGTGGGACTGCTTGATTGAA 420
Db 1208 TTCTTACAAAAGCATTTAGGACTTCATAAAGATTTTATCAGTGGGACTGCTTGATTGAA 1267
QY 421 GGAGATGATGAGATCTTATTCCAGGGACCAACATTTAAACACAACCAATCAACATCATG 480
Db 1268 GGAGATGATGAGATCTTATTCCAGGGACCAACATTTAAACACAACCAATCAACATCATG 1327
QY 481 TTACAGAACTCTTCAGGAATAGAGAAATACAAAT 514
Db 1328 TTACAGAACTCTTCAGGAATAGAGAAATACAAAT 1361

RESULT 3

US-10-406-156-9
; Sequence 9, Application US/10406156
; Publication No. US20030186421A1
; GENERAL INFORMATION:
; APPLICANT: MacPhee, Colin Houston
; Tew, David Graham
; Southan, Christopher Donald
; Hickey, Dierdre Mary Bernadette
; Gloger, Israel Simon
; Lawrence, Geoffrey Mark Prouse
; Rice, Simon Quentyn John
; TITLE OF INVENTION: Compounds
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/406,156
; FILING DATE: 02-Apr-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/569,899
; FILING DATE: 12-May-2000
; APPLICATION NUMBER: 09/294,384
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Dustman, Wayne J.
; REGISTRATION NUMBER: 33,870
; REFERENCE/DOCKET NUMBER: P30693
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5023
; TELEFAX: 610-270-5090
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1361 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 38..1360
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:

US-10-406-156-9
Query Match 100.0%; Score 514; DB 16; Length 1361;
Best Local Similarity 100.0%; Pred. No. 1.7e-127;
Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGACATTTCTTTGGTGAGCAACGGTTATTTCAGACTCTTAGTGAAGATTCAGAGATTTCAGA 60
Db 848 GGACATTTCTTTGGTGAGCAACGGTTATTTCAGACTCTTAGTGAAGATTCAGAGATTTCAGA 907
QY 61 TGTGGTATTGCCCTGGGATGCATGGATGTTTCCACTGGGTGATGAAGTATATTCAGAAATT 120
Db 908 TGTGGTATTGCCCTGGGATGCATGGATGTTTCCACTGGGTGATGAAGTATATTCAGAAATT 967
QY 121 CCTCAGCCCTCTTTTATTCACACTCTGAATATTTCCAAATATCTCTGCTAATATCAAAAA 180
Db 968 CCTCAGCCCTCTTTTATTCACACTCTGAATATTTCCAAATATCTCTGCTAATATCAAAAA 1027
QY 181 ATGAAAAATGCTACTCACCTGATAAAGAAAGAAAGATGATTACAATCAGGGTTTCAGTC 240
Db 1028 ATGAAAAATGCTACTCACCTGATAAAGAAAGAAAGATGATTACAATCAGGGTTTCAGTC 1087
QY 241 CACCAGAAATTTTGTGCTGACTTCACCTTTTGCAACTGGCAAAATAATTGGACACATGCTCAAA 300
Db 1088 CACCAGAAATTTTGTGCTGACTTCACCTTTTGCAACTGGCAAAATAATTGGACACATGCTCAAA 1147
QY 301 TTAAGGGAGACATAGATTCAAATGCAGCTATTGATCTTAGCAACAAGCTTCATTAGCA 360
Db 1148 TTAAGGGAGACATAGATTCAAATGCAGCTATTGATCTTAGCAACAAGCTTCATTAGCA 1207
QY 361 TTCTTACAAAAGCATTTAGGACTTCATAAAGATTTTATCAGTGGGACTGCTTGATTGAA 420
Db 1208 TTCTTACAAAAGCATTTAGGACTTCATAAAGATTTTATCAGTGGGACTGCTTGATTGAA 1267
QY 421 GGAGATGATGAGATCTTATTCCAGGGACCAACATTTAAACACAACCAATCAACATCATG 480
Db 1268 GGAGATGATGAGATCTTATTCCAGGGACCAACATTTAAACACAACCAATCAACATCATG 1327
QY 481 TTACAGAACTCTTCAGGAATAGAGAAATACAAAT 514
Db 1328 TTACAGAACTCTTCAGGAATAGAGAAATACAAAT 1361

RESULT 4

US-09-962-832-110
; Sequence 110, Application US/09962832
; Patent No. US20020110821A1
; GENERAL INFORMATION:
; APPLICANT: Ebner, Reinhard
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
; FILE OF INVENTION: Sets
; FILE REFERENCE: 689290-74
; CURRENT APPLICATION NUMBER: US/09/962,832
; CURRENT FILING DATE: 2001-09-25
; PRIOR FILING DATE: 2000-09-25
; PRIOR FILING DATE: 2000-09-25
; PRIOR FILING DATE: 2000-09-25
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 110
; LENGTH: 1561
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-962-832-110

Query Match 100.0%; Score 514; DB 9; Length 1561;
Best Local Similarity 100.0%; Pred. No. 1.8e-127;
Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGACATTTCTTTGGTGAGCAACGGTTATTTCAGACTCTTAGTGAAGATTCAGAGATTTCAGA 60
Db 1027 GGACATTTCTTTGGTGAGCAACGGTTATTTCAGACTCTTAGTGAAGATTCAGAGATTTCAGA 1086

QY 61 TGTGGTATTCCTGGATGCATGATGTTTCCACTGGGTGATGAAGTATATTCAGAAATT 120
 Db 1087 TGTGGTATTCCTGGATGCATGATGTTTCCACTGGGTGATGAAGTATATTCAGAAATT 1146
 QY 121 CCTCAGCCCTCTTTTATCAACTCTGAATATTCCTGCTGAATATCAATAA 180
 Db 1147 CCTCAGCCCTCTTTTATCAACTCTGAATATTCCTGCTGAATATCAATAA 1206
 QY 181 ATGAATAAATGCTACTCACCTGATGAAGAAAGATGATTAACAATCAGGGTTCAGTC 240
 Db 1207 ATGAATAAATGCTACTCACCTGATGAAGAAAGATGATTAACAATCAGGGTTCAGTC 1266
 QY 241 CACGAGAAATTTGCTGACTTCACTTTTGCACCTGGCAAAATATTTGACACATGCTCAAA 300
 Db 1267 CACGAGAAATTTGCTGACTTCACTTTTGCACCTGGCAAAATATTTGACACATGCTCAAA 1326
 QY 301 TTAAGGGAGACATAGATTTCAATTCAGCTATTCATCTTACGACCAAAAGCTTCATTAAGCA 360
 Db 1327 TTAAGGGAGACATAGATTTCAATTCAGCTATTCATCTTACGACCAAAAGCTTCATTAAGCA 1386
 QY 361 TTCTTACAAAGCAATTTAGGACTTCATAAAGATTTTTCAGTGGGACTGCTTCAATTGAA 420
 Db 1387 TTCTTACAAAGCAATTTAGGACTTCATAAAGATTTTTCAGTGGGACTGCTTCAATTGAA 1446
 QY 421 GGAGATGATGAGATCTTATTTCCAGGACCAACATTAACCAACCAATCAACATCATG 480
 Db 1447 GGAGATGATGAGATCTTATTTCCAGGACCAACATTAACCAACCAATCAACATCATG 1506
 QY 481 TTACAGAACTCTTCAGGAATAGAAATACAATT 514
 Db 1507 TTACAGAACTCTTCAGGAATAGAAATACAATT 1540

RESULT 5

US-10-741-601-89
 ; Sequence 89, Application US/10741601
 ; Publication No. US20040166519A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CARGILL, Michele et al.
 ; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
 ; FILE REFERENCE: CL001500
 ; CURRENT APPLICATION NUMBER: US/10/741.601
 ; CURRENT FILING DATE: 2003-12-22
 ; NUMBER OF SEQ ID NOS: 26415
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 89
 ; LENGTH: 1845
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-741-601-89

Query Match 99.8%; Score 513.2; DB 18; Length 1845;
 Best Local Similarity 99.6%; Pred. No. 3.2e-127;
 Matches 512; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGACATCTTTTGGTGGAGCAACGGTTATTCAGACTCTTTAGTGAAGATCAGAGATTGAGA 60
 Db 989 GGACATCTTTTGGTGGAGCAACGGTTATTCAGACTCTTTAGTGAAGATCAGAGATTGAGA 1048
 QY 61 TGTGGTATTCCTGGATGCATGATGTTTCCACTGGGTGATGAAGTATATTCAGAAATT 120
 Db 1049 TGTGGTATTCCTGGATGCATGATGTTTCCACTGGGTGATGAAGTATATTCAGAAATT 1108
 QY 121 CCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAAATATTCCTGCTGAATATCAATAA 180
 Db 1109 CCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAAATATTCCTGCTGAATATCAATAA 1168
 QY 181 ATGAATAAATGCTACTCACCTGATGAAGAAAGATGATTAACAATCAGGGTTCAGTC 240
 Db 1169 ATGAATAAATGCTACTCACCTGATGAAGAAAGATGATTAACAATCAGGGTTCAGTC 1228

QY 241 CACGAGAAATTTGCTGACTTCACTTTTGCACCTGGCAAAATATTTAGCAACATGCTCAAA 300
 Db 1229 CACGAGAAATTTGCTGACTTCACTTTTGCACCTGGCAAAATATTTAGCAACATGCTCAAA 1288
 QY 301 TTAAGGGAGACATAGATTTCAATTCAGCTATTCATCTTACGACCAAAAGCTTCATTAAGCA 360
 Db 1289 TTAAGGGAGACATAGATTTCAATTCAGCTATTCATCTTACGACCAAAAGCTTCATTAAGCA 1348
 QY 361 TTCTTACAAAGCAATTTAGGACTTCATAAAGATTTTTCAGTGGGACTGCTTCAATTGAA 420
 Db 1349 TTCTTACAAAGCAATTTAGGACTTCATAAAGATTTTTCAGTGGGACTGCTTCAATTGAA 1408
 QY 421 GGAGATGATGAGATCTTATTTCCAGGACCAACATTAACCAACCAATCAACATCATG 480
 Db 1409 GGAGATGATGAGATCTTATTTCCAGGACCAACATTAACCAACCAATCAACATCATG 1468
 QY 481 TTACAGAACTCTTCAGGAATAGAAATACAATT 514
 Db 1469 TTACAGAACTCTTCAGGAATAGAAATACAATT 1502

RESULT 6

US-10-741-601-90
 ; Sequence 90, Application US/10741601
 ; Publication No. US20040166519A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CARGILL, Michele et al.
 ; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
 ; FILE REFERENCE: CL001500
 ; CURRENT APPLICATION NUMBER: US/10/741.601
 ; CURRENT FILING DATE: 2003-12-22
 ; NUMBER OF SEQ ID NOS: 26415
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 90
 ; LENGTH: 1964
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-741-601-90

Query Match 99.8%; Score 513.2; DB 18; Length 1964;
 Best Local Similarity 99.6%; Pred. No. 3.3e-127;
 Matches 512; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGACATCTTTTGGTGGAGCAACGGTTATTCAGACTCTTTAGTGAAGATCAGAGATTGAGA 60
 Db 1108 GGACATCTTTTGGTGGAGCAACGGTTATTCAGACTCTTTAGTGAAGATCAGAGATTGAGA 1167
 QY 61 TGTGGTATTCCTGGATGCATGATGTTTCCACTGGGTGATGAAGTATATTCAGAAATT 120
 Db 1168 TGTGGTATTCCTGGATGCATGATGTTTCCACTGGGTGATGAAGTATATTCAGAAATT 1227
 QY 121 CCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAAATATTCCTGCTGAATATCAATAA 180
 Db 1228 CCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAAATATTCCTGCTGAATATCAATAA 1287
 QY 181 ATGAATAAATGCTACTCACCTGATGAAGAAAGATGATTAACAATCAGGGTTCAGTC 240
 Db 1288 ATGAATAAATGCTACTCACCTGATGAAGAAAGATGATTAACAATCAGGGTTCAGTC 1347
 QY 241 CACGAGAAATTTGCTGACTTCACTTTTGCACCTGGCAAAATATTTAGCAACATGCTCAAA 300
 Db 1348 CACGAGAAATTTGCTGACTTCACTTTTGCACCTGGCAAAATATTTAGCAACATGCTCAAA 1407
 QY 301 TTAAGGGAGACATAGATTTCAATTCAGCTATTCATCTTACGACCAAAAGCTTCATTAAGCA 360
 Db 1408 TTAAGGGAGACATAGATTTCAATTCAGCTATTCATCTTACGACCAAAAGCTTCATTAAGCA 1467
 QY 361 TTCTTACAAAGCAATTTAGGACTTCATAAAGATTTTTCAGTGGGACTGCTTCAATTGAA 420
 Db 1468 TTCTTACAAAGCAATTTAGGACTTCATAAAGATTTTTCAGTGGGACTGCTTCAATTGAA 1527
 QY 421 GGAGATGATGAGAAATCTTATTTCCAGGACCAACATTAACCAACCAATCAACATCATG 480

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Db      1528  GGAGATGATGAGATCTTATTCCAGGAGCAGCAATTTACACACCAATCAACATCATG. 1587
Qy      481  TTACAGAACTCTTCAGGAATAGAGAAATACAAATT 514
Db      1588  TTACAGAACTCTTCAGGAATAGAGAAATACAAATT 1621

RESULT 7
US-10-415-682B-1
; Sequence 1, Application US/10415682B
; Publication No. US20040259087A1
; GENERAL INFORMATION:
; APPLICANT: Campbell, David
; APPLICANT: McGinnis, Ralph
; APPLICANT: Valdes, Ana, Maria
; TITLE OF INVENTION: METHOD AND KIT TO DETERMINE LP-PLA2
; TITLE OF INVENTION: POLYMORPHIC VARIANTS ASSOCIATED WITH SUSCEPTIBILITY TO
; TITLE OF INVENTION: ATHEROSCLEROSIS
; FILE REFERENCE: P32704
; CURRENT APPLICATION NUMBER: US/10/415.682B
; CURRENT FILING DATE: 2003-05-01
; PRIOR APPLICATION NUMBER: PCT/GB01/04876
; PRIOR FILING DATE: 2001-02-11
; PRIOR APPLICATION NUMBER: GB 0027181.7
; PRIOR FILING DATE: 2000-04-11
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1323
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-415-682B-1

Query Match      99.8%; Score 513; DB 18; Length 1323;
Best Local Similarity 100.0%; Pred. No. 3.1e-127; Indels 0; Gaps 0;
Matches 513; Conservative 0; Mismatches 0;

Qy      1      GGACATCTTTTGGTGAGCAACGGTTATTCCAGACTCTTAGTGAAGATTCAGAGATTTCAGA 60
Db      811    GGACATCTTTTGGTGAGCAACGGTTATTCCAGACTCTTAGTGAAGATTCAGAGATTTCAGA 870

Qy      61     TGTGGTATGCCCTGGATGCATGATGTTCCACTGGGTGATGAAGTATATTCAGAAATT 120
Db      871    TGTGGTATGCCCTGGATGCATGATGTTCCACTGGGTGATGAAGTATATTCAGAAATT 930

Qy      121    CCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAAATCTCTGCTTAATATCAATAAA 180
Db      931    CCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAAATCTCTGCTTAATATCAATAAA 990

Qy      181    ATGAAAAAATGCTACTCACCTGATAAAGAAAGAGATGATTACAATCAGGGGTTTCAGTC 240
Db      991    ATGAAAAAATGCTACTCACCTGATAAAGAAAGAGATGATTACAATCAGGGGTTTCAGTC 1050

Qy      241    CACAGAAATTTGCTGACTTCACCTTTGCAACTGGCAAAATAATTTGACACATGCTCAAA 300
Db      1051   CACAGAAATTTGCTGACTTCACCTTTGCAACTGGCAAAATAATTTGACACATGCTCAAA 1110

Qy      301     TTAAGGGAGACATAGATTCAAATGCGACTATTGATCTTAGCAACAAGCTTCATTAGCA 360
Db      1111   TTAAGGGAGACATAGATTCAAATGCGACTATTGATCTTAGCAACAAGCTTCATTAGCA 1170

Qy      361     TTCTTACAAAAGCATTTAGGACTTCATAAAGATTTTGCATGAGGGAGCTGCTTCATTGAA 420
Db      1171   TTCTTACAAAAGCATTTAGGACTTCATAAAGATTTTGCATGAGGGAGCTGCTTCATTGAA 1230

Qy      421     GGAGATGATGAGATCTTTATTCAGGGACCAACATTTAACACAAATCAACATCATG 480
Db      1231   GGAGATGATGAGATCTTTATTCAGGGACCAACATTTAACACAAATCAACATCATG 1290

Qy      481     TTACAGAACTCTTCAGGATAGAGAAATACAAATT 513

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Db      1291  TTACAGAACTCTTCAGGAATAGAGAAATACAAATT 1323

RESULT 8
US-09-729-402-30
; Sequence 30, Application US/09729402
; Patent No. US20010021379A1
; GENERAL INFORMATION:
; APPLICANT: Cousens, Lawrence S.
; Eberhardt, Christine D.
; Gray, Patrick W.
; Le Trong, Hai
; Tjoelker, Larry W.
; Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor
; Acetylhydrolase
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/729,402
; FILING DATE: 04-Dec-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/318,905
; FILING DATE: 06-OCT-1994
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 06-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. US20010021379Aland, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/32793
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3658
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1335 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-09-729-402-30

Query Match      99.7%; Score 512.4; DB 9; Length 1335;
Best Local Similarity 99.8%; Pred. No. 4.5e-127;
Matches 513; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1      GGACATCTTTTGGTGAGCAACGGTTATTCCAGACTCTTAGTGAAGATTCAGAGATTTCAGA 60
Db      811    GGACATCTTTTGGTGAGCAACGGTTATTCCAGACTCTTAGTGAAGATTCAGAGATTTCAGA 870

Qy      61     TGTGGTATGCCCTGGATGCATGATGTTCCACTGGGTGATGAAGTATATTCAGAAATT 120
Db      871    TGTGGTATGCCCTGGATGCATGATGTTCCACTGGGTGATGAAGTATATTCAGAAATT 930

Qy      121    CCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAAATCTCTGCTTAATATCAATAAA 180
Db      931    CCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAAATCTCTGCTTAATATCAATAAA 990

Qy      181    ATGAAAAAATGCTACTCACCTGATAAAGAAAGAGATGATTACAATCAGGGGTTTCAGTC 240

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Db 991 ATGAAAATGCTACTCCTGATGATAAGAAAGAGATGATTACAATCAGGGGTTGAGTC 1050
Qy 241 CACCAGAAATTTGCTGACTTCACTTTTGCACAAATGGAACACATGCTCAAA 300
Db 1051 CACCAGAAATTTGCTGACTTCACTTTTGCACAAATGGAACACATGCTCAAA 1110
Qy 301 TTAAGGAGACATAGATGATCAATGAGCTATTGATCTTAGCAACAAAGCTTCATTAGCA 360
Db 1111 TTAAGGAGACATAGATGATCAATGAGCTATTGATCTTAGCAACAAAGCTTCATTAGCA 1170
Qy 361 TTCTTACAAAGCAATTTAGGACTTCATTAAGATTTTGTGATGAGCTGGGCTGCTTGAATGAA 420
Db 1171 TTCTTACAAAGCAATTTAGGACTTCATTAAGATTTTGTGATGAGCTGGGCTGCTTGAATGAA 1230
Qy 421 GGAGATGATGAGAAATCTTATTCCAGGAGCAACCAATTAACACAAATCAACATCATG 480
Db 1231 GGAGATGATGAGAAATCTTATTCCAGGAGCAACCAATTAACACAAATCAACATCATG 1290
Qy 481 TTACAGAACTTTCAGGAATAGAAATACAAAT 514
Db 1291 TTACAGAACTTTCAGGAATAGAAATACAAAT 1324

RESULT 9

US-10-003-978A-30
; Sequence 30, Application US/10003978A
; Publication No. US2003007247A1

GENERAL INFORMATION:

APPLICANT: Cousens, Lawrence S.
Eberhardt, Christine D.
Gray, Patrick W.
Le Trong, Hai
Tjoelker, Larry W.
Wilder, Cheryl L.

TITLE OF INVENTION: Platelet-Activating Factor
Acetylhydrolase

NUMBER OF SEQUENCES: 30

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, Gerstein & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois

COUNTRY: United States of America
ZIP: 60606-6357

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/003,978A

FILING DATE: 23-Oct-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/729,402

FILING DATE: 04-DEC-2000

APPLICATION NUMBER: US 09/577,758

FILING DATE: 23-MAY-2000

APPLICATION NUMBER: US 09/010,715

FILING DATE: 22-JAN-1998

APPLICATION NUMBER: US 08/480,658

FILING DATE: 07-JUN-1995

APPLICATION NUMBER: US 08/318,905

FILING DATE: 06-OCT-1994

APPLICATION NUMBER: US 08/133,803

FILING DATE: 06-OCT-1993

ATTORNEY/AGENT INFORMATION:

NAME: No. US2003007247Aland, Greta E.
REGISTRATION NUMBER: 35,302

REFERENCE/DOCKET NUMBER: 27866/37792

TELECOMMUNICATION INFORMATION:

TELEPHONE: (312) 474-6300

TELEFAX: (312) 474-0448

INFORMATION FOR SEQ ID NO: 30:

SEQUENCE CHARACTERISTICS:

LENGTH: 1335 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

SEQUENCE DESCRIPTION: SEQ ID NO: 30:

US-10-003-978A-30

Query Match

Best Local Similarity 99.8%; Score 512.4; DB 14; Length 1335;

Matches 513; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGACATCTCTTTGGTGAGCAACGGTTATTTCAGACTCTTAGTCAAGATCAGAGATTGAGA 60
Db 811 GGACATCTCTTTGGTGAGCAACGGTTATTTCAGACTCTTAGTCAAGATCAGAGATTGAGA 870
Qy 61 TGTGGTATTGCCCTGGATGATGATGTTTCCACTGGGTGATGAAGTATATTCAGAAAT 120
Db 871 TGTGGTATTGCCCTGGATGATGATGTTTCCACTGGGTGATGAAGTATATTCAGAAAT 930
Qy 121 CCTCAGCCCTCTTTTTCATCAACTCTGAATATTTTCCAATATCTCTCTAATATCATAAAA 180
Db 931 CCTCAGCCCTCTTTTTCATCAACTCTGAATATTTTCCAATATCTCTCTAATATCATAAAA 990
Qy 181 ATGAAAAATGCTACTCCTGATTAAGAAAGAAAGATGATTAACATCAGGGGTTGAGTC 240
Db 991 ATGAAAAATGCTACTCCTGATTAAGAAAGAAAGATGATTAACATCAGGGGTTGAGTC 1050
Qy 241 CACCAGAAATTTGCTGACTTCACTTTTGGCAACTGGCAAAATAATTTGGACACATGCTCAAA 300
Db 1051 CACCAGAAATTTGCTGACTTCACTTTTGGCAACTGGCAAAATAATTTGGACACATGCTCAAA 1110
Qy 301 TTAAGGGAGACATAGATTCAAATGAGCTATTGATCTTAGCAACAAAGCTTCATTAGCA 360
Db 1111 TTAAGGGAGACATAGATTCAAATGAGCTATTGATCTTAGCAACAAAGCTTCATTAGCA 1170
Qy 361 TTCTTACAAAGCAATTTAGGACTTTCATTAAGATTTTGTGATGAGCTGGGCTGCTTGAATGAA 420
Db 1171 TTCTTACAAAGCAATTTAGGACTTTCATTAAGATTTTGTGATGAGCTGGGCTGCTTGAATGAA 1230
Qy 421 GGAGATGATGAGAAATCTTATTCCAGGGAGCAACATTAACACAAATCAACATCATG 480
Db 1231 GGAGATGATGAGAAATCTTATTCCAGGGAGCAACATTAACACAAATCAACATCATG 1290
Qy 481 TTACAGAACTTTCAGGAATAGAAATACAAAT 514
Db 1291 TTACAGAACTTTCAGGAATAGAAATACAAAT 1324

RESULT 10

US-10-172-118-1120

; Sequence 1120, Application US/10172118

; Publication No. US20030224374A1

GENERAL INFORMATION:

APPLICANT: Dai, Hongyue

APPLICANT: He, Yudong

APPLICANT: Linsley, Peter

APPLICANT: Mao, Mao

APPLICANT: Roberts, Chris

APPLICANT: Van 't Veer, Laura

APPLICANT: Van de Vijver, Marc

APPLICANT: Bernards, Rene

TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients

FILE REFERENCE: 9301-175-999

CURRENT APPLICATION NUMBER: US/10/172,118

CURRENT FILING DATE: 2002-06-14

PRIOR APPLICATION NUMBER: 60/380,770

PRIOR FILING DATE: 2002-05-14

NUMBER OF SEQ ID NOS: 2699

SEQ ID NO 1120

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; LENGTH: 1505
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NM_005084
; DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-1120

Query Match          99.7%; Score 512.4; DB 17; Length 1505;
Best Local Similarity 99.8%; Pred. No. 4.8e-127;
Matches 513; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGACATCTCTTTTGGTGAGCAACGGTTATTTCAGACTCTTAGTGAAGATTCAGAGATTTCAGA 60
Db 972 GGACATCTCTTTTGGTGAGCAACGGTTATTTCAGACTCTTAGTGAAGATTCAGAGATTTCAGA 1031
Qy 61 TGTGGTATTGCCCTGGATGATGTTTCCACTGGGTGATGAAGTATATTCAGAGATT 120
Db 1032 TGTGGTATTGCCCTGGATGATGTTTCCACTGGGTGATGAAGTATATTCAGAGATT 1091
Qy 121 CCTCAGCCCTCTTTTATCAACTCTGAATATTTTCCAATATCTGCTTAATATCATATAAA 180
Db 1092 CCTCAGCCCTCTTTTATCAACTCTGAATATTTTCCAATATCTGCTTAATATCATATAAA 1151
Qy 181 ATGAAAAATCTACTCACCTGATAAAGAAAGAAAGATGATTACAATCAGGGGTTTCAGTC 240
Db 1152 ATGAAAAATCTACTCACCTGATAAAGAAAGAAAGATGATTACAATCAGGGGTTTCAGTC 1211
Qy 241 CACCAGAAATTTGCTGACTTCACTTTTGCACCTGGCAAAATAATTTGGACACATGCTCAAA 300
Db 1212 CACCAGAAATTTGCTGACTTCACTTTTGCACCTGGCAAAATAATTTGGACACATGCTCAAA 1271
Qy 301 TTAAGGGAGACATAGATTCAAAATGCACTATTGATCTTAGCAACAAAGCTTCATTAGCA 360
Db 1272 TTAAGGGAGACATAGATTCAAAATGCACTATTGATCTTAGCAACAAAGCTTCATTAGCA 1331
Qy 361 TTCTTACAAAAGCAATTTAGGACTTCATAAAGATTTTGCATGAGTGGAGCTGCTTGAATGAA 420
Db 1332 TTCTTACAAAAGCAATTTAGGACTTCATAAAGATTTTGCATGAGTGGAGCTGCTTGAATGAA 1391
Qy 421 GGAGATGATGAGATCTTTATTCCAGGGACCAACATTAAACAAACCAATCAACACATCATG 480
Db 1392 GGAGATGATGAGATCTTTATTCCAGGGACCAACATTAAACAAACCAATCAACACATCATG 1451
Qy 481 TTACAGAACTCTTCAGGAATAGAGAAATACAAATT 514
Db 1452 TTACAGAACTCTTCAGGAATAGAGAAATACAAATT 1485

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RESULT 11

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US-10-342-887-1120
; Sequence 1120, Application US/10342887
; Publication No. US20040058340A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter S.
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Christopher J.
; APPLICANT: Van 't Veer, Laura Johanna
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-188-999
; CURRENT APPLICATION NUMBER: US/10/342,887
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: 60/298,918
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/380,710
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 10/172,118
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 2699

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; SEQ ID NO 1120
; LENGTH: 1505
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-342-887-1120

Query Match          99.7%; Score 512.4; DB 17; Length 1505;
Best Local Similarity 99.8%; Pred. No. 4.8e-127;
Matches 513; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGACATCTCTTTTGGTGAGCAACGGTTATTTCAGACTCTTAGTGAAGATTCAGAGATTTCAGA 60
Db 972 GGACATCTCTTTTGGTGAGCAACGGTTATTTCAGACTCTTAGTGAAGATTCAGAGATTTCAGA 1031
Qy 61 TGTGGTATTGCCCTGGATGATGTTTCCACTGGGTGATGAAGTATATTCAGAGATT 120
Db 1032 TGTGGTATTGCCCTGGATGATGTTTCCACTGGGTGATGAAGTATATTCAGAGATT 1091
Qy 121 CCTCAGCCCTCTTTTATCAACTCTGAATATTTTCCAATATCTGCTTAATATCATATAAA 180
Db 1092 CCTCAGCCCTCTTTTATCAACTCTGAATATTTTCCAATATCTGCTTAATATCATATAAA 1151
Qy 181 ATGAAAAATCTACTCACCTGATAAAGAAAGAAAGATGATTACAATCAGGGGTTTCAGTC 240
Db 1152 ATGAAAAATCTACTCACCTGATAAAGAAAGAAAGATGATTACAATCAGGGGTTTCAGTC 1211
Qy 241 CACCAGAAATTTGCTGACTTCACTTTTGCACCTGGCAAAATAATTTGGACACATGCTCAAA 300
Db 1212 CACCAGAAATTTGCTGACTTCACTTTTGCACCTGGCAAAATAATTTGGACACATGCTCAAA 1271
Qy 301 TTAAGGGAGACATAGATTCAAAATGCACTATTGATCTTAGCAACAAAGCTTCATTAGCA 360
Db 1272 TTAAGGGAGACATAGATTCAAAATGCACTATTGATCTTAGCAACAAAGCTTCATTAGCA 1331
Qy 361 TTCTTACAAAAGCAATTTAGGACTTCATAAAGATTTTGCATGAGTGGAGCTGCTTGAATGAA 420
Db 1332 TTCTTACAAAAGCAATTTAGGACTTCATAAAGATTTTGCATGAGTGGAGCTGCTTGAATGAA 1391
Qy 421 GGAGATGATGAGATCTTTATTCCAGGGACCAACATTAAACAAACCAATCAACACATCATG 480
Db 1392 GGAGATGATGAGATCTTTATTCCAGGGACCAACATTAAACAAACCAATCAACACATCATG 1451
Qy 481 TTACAGAACTCTTCAGGAATAGAGAAATACAAATT 514
Db 1452 TTACAGAACTCTTCAGGAATAGAGAAATACAAATT 1485

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RESULT 12

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US-10-755-889-277
; Sequence 277, Application US/10755889
; Publication No. US20040171823A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-kB
; FILE REFERENCE: D0284 NP
; CURRENT APPLICATION NUMBER: US/10/755,889
; CURRENT FILING DATE: 2004-01-13
; PRIOR APPLICATION NUMBER: U.S. 60/440,068
; PRIOR FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: U.S. 60/469,757
; PRIOR FILING DATE: 2003-05-12
; NUMBER OF SEQ ID NOS: 823
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 277
; LENGTH: 1505
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-755-889-277

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Query Match          99.7%; Score 512.4; DB 18; Length 1505;
Best Local Similarity 99.8%; Pred. No. 4.8e-127;
Matches 513; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```


TITLE OF INVENTION: Platelet-Activating Factor
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, Gerstein & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6357
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/003,978A
FILING DATE: 23-Oct-2001
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/729,402
FILING DATE: 04-DEC-2000
APPLICATION NUMBER: US 09/577,758
FILING DATE: 23-MAY-2000
APPLICATION NUMBER: US 09/010,715
FILING DATE: 22-JAN-1998
APPLICATION NUMBER: US 08/480,658
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/318,905
FILING DATE: 06-OCT-1994
APPLICATION NUMBER: US 08/133,803
FILING DATE: 06-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: No. US20030072747A1and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/37792
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1520 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 162..1484
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-003-978A-7

Query Match 99.7%; Score 512.4; DB 14; Length 1520;
Best Local Similarity 99.8%; Pred. No. 4.8e-127;
Matches 513; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GGACATCTTTTGGTGGAGCAACGGTTATTGAGATCTTTAGTGAAGATCAGAGATTGAGA 60
Db 972 GGACATCTTTTGGTGGAGCAACGGTTATTGAGATCTTTAGTGAAGATCAGAGATTGAGA 1031
Qy 61 TGTGGTATTCCTGGATGCATGATGTTTCCACTGGGTGATGAAGTATATTCAGAAATT 120
Db 1032 TGTGGTATTCCTGGATGCATGATGTTTCCACTGGGTGATGAAGTATATTCAGAAATT 1091
Qy 121 CCTCAGCCCTCTTTTATCACTCTGAAATTTTCAATATCTGCTAAATATCAATAA 180
Db 1092 CCTCAGCCCTCTTTTATCACTCTGAAATTTTCAATATCTGCTAAATATCAATAA 1151
Qy 181 ATGAAAAATGCTACTCACCCTGATAAAGAAAGAGATGATTACAATCAGGGGTTGAGTC 240
Db 1152 ATGAAAAATGCTACTCACCCTGATAAAGAAAGAGATGATTACAATCAGGGGTTGAGTC 1211
Qy 241 CACCAGAAATTTTGTGCTGACTTCACCTTTTGCACATGCGCAAAATAATTGGACATGCTCAAA 300

Db 1212 CACCAGAAATTTTGTGCTGACTTCACCTTTTGCACATGCGCAAAATAATTGGACATGCTCAAA 1271
Qy 301 TTAAGGGAGACATAGATTCAAATGCACTGATTTAGCAACAAAGCTTTCATTAGCA 360
Db 1272 TTAAGGGAGACATAGATTCAAATGCACTGATTTAGCAACAAAGCTTTCATTAGCA 1331
Qy 361 TTCTTACAAAAGCATTAGGACTTCATAAAGATTTTGCATCAGTGGGACTGCTTGAATGAA 420
Db 1332 TTCTTACAAAAGCATTAGGACTTCATAAAGATTTTGCATCAGTGGGACTGCTTGAATGAA 1391
Qy 421 GGAGATGATCAGAAATCTTTTCCAGGGACCAACATTAACACCAATCAACACATCATG 480
Db 1392 GGAGATGATCAGAAATCTTTTCCAGGGACCAACATTAACACCAATCAACACATCATG 1451
Qy 481 TTACAGAACTCTTCAGGAATAGAGAAATACAATT 514
Db 1452 TTACAGAACTCTTCAGGAATAGAGAAATACAATT 1485
RESULT 15
US-09-922-067f-8
Sequence 8, Application US/09922067
Patent No. US20020177209A1
GENERAL INFORMATION:
APPLICANT: MacPhee, Colin Houston
Tew, David Graham
Southan, Christopher Donald
Hickey, Dierdre Mary Bernadette
Gloger, Israel Simon
Lawrence, Geoffrey Mark Prouse
Rice, Simon Quentyn John
TITLE OF INVENTION: Lipoprotein Associated Phospholipase A2, Inhibitors
Thereof And Use Of The Same In Diagnosis And Therapy
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/922,067
FILING DATE: 03-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/193,130
FILING DATE: 1998-11-17
APPLICATION NUMBER: PCT/GB94/01374
FILING DATE: 24 June 1994
NAME: Dustman, Wayne J.
REGISTRATION NUMBER: 33,870
REFERENCE/DOCKET NUMBER: P30693
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5023
TELEFAX: 610-270-5090
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 572 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO

SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-922-067-8

Query Match 99.1%; Score 509.2; DB 9; Length 572;
Best Local Similarity 99.4%; Pred. No. 2.2e-126;
Matches 511; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy	1	GGACATTCCTTTGGTGGAGCAACGGTTATTACAGACTCTTAGTGAAGATCAGAGATTTCAGA	60
Db	16	GGACATTCCTTTAGGTGGAGCAACGGTTATTACAGACTCTTAGTGAAGATCAGAGATTTCAGA	75
Qy	61	TGTGTATTGGCCCTGCGATGCGATGTTCCACCTGGGTGATGAAGTATATCCAGATT	120
Db	76	TGTGTATTGGCCCTGCGATGCGATGTTCCACCTGGGTGATGAAGTATATCCAGATT	135
Qy	121	CCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAATATCTCTGCTAATATCATATAA	180
Db	136	CCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAATATCTCTGCTAATATCATATAA	195
Qy	181	ATGAATAAATCTACTACCTGATTAAGAAAGAAAGATGATTACAATCAGGGGTTTCAGTC	240
Db	196	ATGAATAAATCTACTACCTGATTAAGAAAGAAAGATGATTACAATCAGGGGTTTCAGTC	255
Qy	241	CACCAGAAATTTGCTGACTTCACCTTTTGCACCTGGCAAAATAATTGGACACATGCTCAA	300
Db	256	CACCAGAAATTTGCTGACTTCACCTTTTGCACCTGGCAAAATAATTGGACACATGCTCAA	315
Qy	301	TTAAAGGGAGACATAGATTCAAATGCAGCTATTGATCTTAGCAACAAAGCTTCATTAGCA	360
Db	316	TTAAAGGGAGACATAGATTCAAATGCAGCTATTGATCTTAGCAACAAAGCTTCATTAGCA	375
Qy	361	TTCTTACAAAGCATTTAGGACTTCATAAGATTTTGTATCAGTGGGACTGCTTGATTGAA	420
Db	376	TTCTTACAAAGCATTTAGGACTTCATAAGATTTTGTATCAGTGGGACTGCTTGATTGAA	435
Qy	421	GGAGATGATGAGAAATCTTATTCCAGGGACCAACATTAAACACCAATCAACACATCATG	480
Db	436	GGAGATGATGAGAAATCTTATTCCAGGGACCAACATTAAACACCAATCAACACATCATG	495
Qy	481	TTACAGAACTCTTCAGGAATAGAGAAATACAATT	514
Db	496	TTACAGAACTCTTCAGGAATAGAGAAATACAATT	529

Search completed: March 16, 2005, 06:35:28
Job time : 502.116 Secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 15, 2005, 09:15:21 ; Search time 2076.29 Seconds
(without alignment)
9423.093 Million cell updates/sec

Title: US-09-922-067f-9_COPY_848_1361
Perfect score: 514
Sequence: 1 ggcacattcttttggtagc.....aggaaatagagaatacaatt 514

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST.*
1: gb_est1.*
2: gb_est2.*
3: gb_hic.*
4: gb_est3.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_gest1.*
9: gb_gest2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	514	100.0	560	4	BM788963
2	514	100.0	650	1	AI343491
3	514	100.0	734	6	CA312081
4	514	100.0	1326	9	AY407445
5	513	99.8	598	2	BF509203
6	510.8	99.4	1326	9	AY407446
7	504.4	98.1	1562	3	CR608325
8	503	97.9	1793	3	BC025674
9	499.4	97.2	1531	3	CR615354
10	498.6	97.0	1022	1	AL575852
11	497.4	96.8	519	2	AW071677
12	475.8	92.6	560	2	BF508812
13	467	90.9	505	5	BQ011547
14	465.8	90.6	818	5	BX330257
15	459	89.3	946	1	AL573565
16	412.2	80.2	900	4	BG530083
17	402	78.2	684	7	CR943719
18	398.8	77.6	677	7	CR950137
19	390.2	75.9	420	1	AA302965
20	384	74.7	689	5	BQ603958
21	383	74.5	619	7	CR953402
22	370	72.0	394	1	AI177011
23	364	70.8	593	7	CR954423
24	360.2	70.1	551	4	BM537293

C 25	354.2	68.9	405	6	CA436968
C 26	354	68.9	574	6	CB471515
C 27	350.6	68.2	622	4	BM536645
C 28	322.4	62.7	513	2	AW950435
C 29	306	59.5	594	7	CK622757
C 30	306	59.5	1326	9	AY407447
C 31	306	59.5	1695	3	AK05210
C 32	306	59.5	1890	3	AK051454
C 33	302.8	58.9	379	1	AA297235
C 34	299.2	58.2	807	6	CA509646
C 35	298.6	58.1	508	1	AJ695792
C 36	297.2	57.8	798	7	CK129701
C 37	292.4	56.9	733	4	BI691924
C 38	291.6	56.7	392	4	BI336794
C 39	289.8	56.4	743	6	CD363890
C 40	288.4	56.1	678	5	CD364088
C 41	288.2	56.1	796	5	BX926110
C 42	277.6	54.0	715	2	AW556825
C 43	273.8	53.3	811	7	CK031981
C 44	273	53.1	542	7	CK953363
C 45	272	52.9	914	7	CK023311

ALIGNMENTS

RESULT 1
BM788963
LOCUS
DEFINITION BM788963 560 bp mRNA linear EST 05-MAR-2002
5', mRNA sequence.
K-EST0068255 S19N665307 Homo sapiens cDNA clone S19N665307-2-H03
ACCSSION BM788963
VERSION BM788963.1 GI:19137195
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 560)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.
TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 2 row: H column: 03
High quality sequence stop: 560.
Location/Qualifiers
1..560
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S19N665307-2-H03"
/sex="M"
/lab_host="Top10P"
/clone_lib="S19N665307"
/note="Organ: Stomach; Vector: pCNS; Site 1: EcoRI;
Site 2: NotI; The poly (A) + RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then decapped
with tabacco acid pyrophosphatase (TAP). The decapped
intact mRNA was ligated with DNA-RNA linker including EcoR
I site by treatment of 14 RNA ligase and the first strand
cDNA was synthesized from oligo dt-selected mRNA by
priming with dt-tailed vector. The dt-tailed vector was
adjusted to have about 60nt. The cDNA vector was
circularized with E. coli DNA ligase after digestion of
EcoRI which site is also included in vector. An RNA strand

BM788963 560 bp mRNA linear EST 05-MAR-2002
K-EST0068255 S19N665307 Homo sapiens cDNA clone S19N665307-2-H03
5', mRNA sequence.
ACCSSION BM788963
VERSION BM788963.1 GI:19137195
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 560)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.
TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 2 row: H column: 03
High quality sequence stop: 560.
Location/Qualifiers
1..560
/organism="Homo sapiens"
/mol_type="mRNA"
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/clone="S19N665307-2-H03"
/sex="M"
/lab_host="Top10P"
/clone_lib="S19N665307"
/note="Organ: Stomach; Vector: pCNS; Site 1: EcoRI;
Site 2: NotI; The poly (A) + RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then decapped
with tabacco acid pyrophosphatase (TAP). The decapped
intact mRNA was ligated with DNA-RNA linker including EcoR
I site by treatment of 14 RNA ligase and the first strand
cDNA was synthesized from oligo dt-selected mRNA by
priming with dt-tailed vector. The dt-tailed vector was
adjusted to have about 60nt. The cDNA vector was
circularized with E. coli DNA ligase after digestion of
EcoRI which site is also included in vector. An RNA strand

converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10⁺ by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

ORIGIN

Query Match 100.0%; Score 514; DB 4; Length 560;
 Best Local Similarity 100.0%; Pred. No. 1.1e-123;
 Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGACATCTTTTGGGAGCAACGGTTATTCAGACTCTTAGTGAAGATCAGAGATTCAGA 60
 DB 25 GGACATCTTTTGGGAGCAACGGTTATTCAGACTCTTAGTGAAGATCAGAGATTCAGA 84

QY 61 TGTGTTATTCCTGCTGATGATGATGTTTCCACTGGGTGATGAAGTATATTCAGAAAT 120
 DB 85 TGTGTTATTCCTGCTGATGATGATGTTTCCACTGGGTGATGAAGTATATTCAGAAAT 144

QY 121 CCTCAGCCCTCTTTTATCAACTCTCAATATTTCCAAATATCCTGCTTAATCATATAA 180
 DB 145 CCTCAGCCCTCTTTTATCAACTCTCAATATTTCCAAATATCCTGCTTAATCATATAA 204

QY 181 ATGAAAATGCTACTCCTGATTAAGAAAGAAAGATGATTAATCAGGGTTCAGTC 240
 DB 205 ATGAAAATGCTACTCCTGATTAAGAAAGAAAGATGATTAATCAGGGTTCAGTC 264

QY 241 CACCAGAAATTTGCTGACTTCACTTTTGCACCTGCAAAATAATTTGGACACATGCTCAA 300
 DB 265 CACCAGAAATTTGCTGACTTCACTTTTGCACCTGCAAAATAATTTGGACACATGCTCAA 324

QY 301 TTAAGGAGACATAGATTTCAATGCTAGTATTTAGCAACAAAGCTTCATTAGCA 360
 DB 325 TTAAGGAGACATAGATTTCAATGCTAGTATTTAGCAACAAAGCTTCATTAGCA 384

QY 361 TTCTTACAAAGCAATTTAGGACTTCATAAAGATTTTGAATGCTGGAGTCTTGAATGAA 420
 DB 385 TTCTTACAAAGCAATTTAGGACTTCATAAAGATTTTGAATGCTGGAGTCTTGAATGAA 444

QY 421 GGAGATGATGAGATCTTTATTCAGGAGCAACCAATTAACCAACCAATCAACATCATG 480
 DB 445 GGAGATGATGAGATCTTTATTCAGGAGCAACCAATTAACCAACCAATCAACATCATG 504

QY 481 TTACAGAACTCTTCAGAAATGAGAAATACAAAT 514
 DB 505 TTACAGAACTCTTCAGAAATGAGAAATACAAAT 538

RESULT 2

AI343491/c
 LOCUS
 DEFINITION
 similar to SW:PAFA_HUMAN Q13093 PLATELET-ACTIVATING FACTOR
 ACETYLHYDROLASE PRECURSOR ; mRNA sequence.

AI343491
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens (human)

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

AI343491 650 bp mRNA linear EST 08-APR-1999
 tb97C04.x1 NCI CGAP Col6 Homo sapiens cDNA clone IMAGE:2062278 3'
 similar to SW:PAFA_HUMAN Q13093 PLATELET-ACTIVATING FACTOR
 ACETYLHYDROLASE PRECURSOR ; mRNA sequence.

AI343491.1 GI:4080697
 EST.
 Homo sapiens (human)

1. (bases 1 to 650)
 NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)

Contact: Robert Strausberg, Ph.D.
 Email: cgapsb@mail.nih.gov
 Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck,
 M.D., Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CCAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
 Insert Length: 785 Std Error: 0.00
 Seq primer: -40UP from Gibco
 High quality sequence stop: 439.

FEATURES

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 Location/Qualifiers
 1..650
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 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:2062278"
 /tissue_type="colon tumor, RER+"
 /lab host="DH10B"
 /clone lib="NCI CGAP Col6"
 /note="Organ: colon; Vector: p773D-Pac (Pharmacia) with a modified polylinker; Site 1: Not 1; Site 2: Eco RI; Plasmid DNA from the normalized library NCI CGAP Col6 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clones 1057416-1061255, and 1144584-1145351).
 Subtraction by Bento Soares and M. Fatima Bonaudo."

ORIGIN

Query Match 100.0%; Score 514; DB 1; Length 650;
 Best Local Similarity 100.0%; Pred. No. 1.2e-123;
 Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGACATCTTTTGGTGGAGCAACGGTTATTCAGACTCTTAGTGAAGATCAGAGATTCAGA 60
 DB 544 GGACATCTTTTGGTGGAGCAACGGTTATTCAGACTCTTAGTGAAGATCAGAGATTCAGA 485

QY 61 TGTGTTATTCCTGCTGATGATGATGTTTCCACTGGGTGATGAAGTATATTCAGAAAT 120
 DB 484 TGTGTTATTCCTGCTGATGATGATGTTTCCACTGGGTGATGAAGTATATTCAGAAAT 425

QY 121 CCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAAATATCTGCTTAATCATATAA 180
 DB 424 CCTCAGCCCTCTTTTATCAACTCTGAATATTTCCAAATATCTGCTTAATCATATAA 365

QY 181 ATGAAAATGCTACTCCTGATTAAGAAAGAAAGATGATTAATCAGGGTTCAGTC 240
 DB 364 ATGAAAATGCTACTCCTGATTAAGAAAGAAAGATGATTAATCAGGGTTCAGTC 305

QY 241 CACCAGAAATTTGCTGACTTCACTTTTGCACCTGGCAAAATAATTTGGACACATGCTCAA 300
 DB 304 CACCAGAAATTTGCTGACTTCACTTTTGCACCTGGCAAAATAATTTGGACACATGCTCAA 245

QY 301 TTAAGGAGACATAGATTTCAATGCTAGTATTTAGCAACAAAGCTTCATTAGCA 360
 DB 244 TTAAGGAGACATAGATTTCAATGCTAGTATTTAGCAACAAAGCTTCATTAGCA 185

QY 361 TTCTTACAAAGCAATTTAGGACTTCATAAAGATTTTGAATGCTGGAGTCTTGAATGAA 420
 DB 184 TTCTTACAAAGCAATTTAGGACTTCATAAAGATTTTGAATGCTGGAGTCTTGAATGAA 125

QY 421 GGAGATGATGAGATCTTTATTCAGGAGCAACCAATTAACCAACCAATCAACATCATG 480
 DB 124 GGAGATGATGAGATCTTTATTCAGGAGCAACCAATTAACCAACCAATCAACATCATG 65

QY 481 TTACAGAACTCTTCAGAAATGAGAAATACAAAT 514
 DB 64 TTACAGAACTCTTCAGAAATGAGAAATACAAAT 31

RESULT 3

CA312081/c
 LOCUS
 DEFINITION
 ACCESSION

CA312081 734 bp mRNA linear EST 04-NOV-2002
 UI-CF-FNO-afj-b-19-0-UI.s1 UI-CF-FNO Homo sapiens cDNA clone
 UI-CF-FNO-afj-b-19-0-UI 3', mRNA sequence.
 CA312081

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VERSION CA312081.1 GI:24530179
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 734)
JOURNAL Bonaldo,M.F., Lennon,G. and Soares,M.B.
PUBMED Normalization and subtraction: two approaches to facilitate gene
COMMENT Genome Res. 6 (9), 791-806 (1996)
9704477
889548
Contact: McCray, PB
University of Iowa
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.reagen.com) or from Open Biosystems
(www.openbiosystems.com).
The following repetitive elements were found in this cDNA
sequence: 1-24, >AT rich#Low_complexity (matched complement)
Seq primer: M13 FORWARD
POLYA=yes.
FEATURES
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/db_xref="taxon:9606"
/clone="UI-CF-FNO-afj-b-19-0-UI"
/tissue_type="Human Lung Epithelial cells"
/lab_host="DHI0B (Life Technologies) (T1 phase resistant)"
/clone_lib="UI-CF-FNO"
/notes="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
UI-CF-FNO is a subtracted cDNA library derived from two
normalized human lung epithelial cell libraries (EN1 and
DUI1). The library was subtracted according to according to
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. For additional information, contact:
bento-soares@uiowa.edu
TAG_TISSUE=Lung Epithelial Cells Tissue nos 359-368
TAG_LIB=UI-CF-FNO
TAG_SEQ=GGCTGTAGGC"
ORIGIN
Query Match 100.0%; Score 514; DB 6; Length 734;
Best Local Similarity 100.0%; Pred. No. 1.2e-123;
Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGACATCTTTTGGTGGAGCAACGGTATTTCAGACTCTTAGTGAAGATCAGAGATTTCAGA 60
DB 552 GGACATCTTTTGGTGGAGCAACGGTATTTCAGACTCTTAGTGAAGATCAGAGATTTCAGA 493
QY 61 TGTGTTATTCCTGGATGCATGGATGTTTCCACTGGGTGATGAAGTATATTTCCAGAAATT 120
DB 492 TGTGTTATTCCTGGATGCATGGATGTTTCCACTGGGTGATGAAGTATATTTCCAGAAATT 433
QY 121 CCTGAGCCCTCTTTTATCATCACTCTGAATATTTCCAAATATTCCTGCTAAATCATATAAA 180
DB 432 CCTGAGCCCTCTTTTATCACTCTGAATATTTCCAAATATTCCTGCTAAATCATATAAA 373
QY 181 ATGAATAATGCTACTCCACCTGATAAAGAAAGAGATGATTACAAATCAGGGGTTTCAGTC 240
DB 372 ATGAATAATGCTACTCCACCTGATAAAGAAAGAGATGATTACAAATCAGGGGTTTCAGTC 313
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QY 241 CACCAGAAATTTGCTGACTTCACCTTTTGCRACTGGCAAAATAATTTGGACATGCTCAA 300
DB 312 CACCAGAAATTTGCTGACTTCACCTTTTGCRACTGGCAAAATAATTTGGACATGCTCAA 253
QY 301 TTAAGGGAGACATAGATTTCAAATGCAGCTATTGATCTTAGCAACAAAGCTTCATTAGCA 360
DB 252 TTAAGGGAGACATAGATTTCAAATGCAGCTATTGATCTTAGCAACAAAGCTTCATTAGCA 193
QY 361 TTCTTACAAAAGCAATTTAGGACTTCATAAAGATTTTGTATCATGTTGGAGCTGTTGATTGAA 420
DB 192 TTCTTACAAAAGCAATTTAGGACTTCATAAAGATTTTGTATCATGTTGGAGCTGTTGATTGAA 133
QY 421 GGAGATGATGAGATCTTATTTCCAGGGGACCAACATTAACACAACTCAACACATCATG 480
DB 132 GGAGATGATGAGATCTTATTTCCAGGGGACCAACATTAACACAACTCAACACATCATG 73
QY 481 TTACAGAACTCTTCAGGAATAGAGAAATACAAATT 514
DB 72 TTACAGAACTCTTCAGGAATAGAGAAATACAAATT 39
RESULT 4
LOCUS AY407445 1326 bp DNA linear GSS 15-DEC-2003
DEFINITION Homo sapiens PLA2G7 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION AY407445
VERSION AY407445.1 GI:39763416
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1326)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 1326)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
source Location/Qualifiers
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Query Match 100.0%; Score 514; DB 9; Length 1326;
Best Local Similarity 100.0%; Pred. No. 1.4e-123;
Matches 514; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGACATCTTTTGGTGGAGCAACGGTATTTCAGACTCTTAGTGAAGATCAGAGATTTCAGA 60
DB 811 GGACATCTTTTGGTGGAGCAACGGTATTTCAGACTCTTAGTGAAGATCAGAGATTTCAGA 870
QY 61 TGTGTTATTCCTGGATGCATGGATGTTTCCACTGGGTGATGAAGTATATTTCCAGAAATT 120
DB 871 TGTGTTATTCCTGGATGCATGGATGTTTCCACTGGGTGATGAAGTATATTTCCAGAAATT 930
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Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Perriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
Science 302 (5652), 1960-1963 (2003)
14671302
2 (bases 1 to 1326)
Clark,A.G., Gianowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Perriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
Location/Qualifiers
source
1..1326
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
<1..>1326
/gene="PLA2G7"
/locus_tag="HCM2893"
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Query Match 99.4%; Score 510.8; DB 9; Length 1326;
Best Local Similarity 99.6%; Pred. No. 9.3e-123;
Matches 512; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 GGACATCTTTTGGTGAGCAACGGTTATTAGAGTCTTAGTGAAGATTCAGATTTCAGA 60
Db 811 GGACATCTTTTGGTGAGCAACGGTTATTAGAGTCTTAGTGAAGATTCAGATTTCAGA 870
Qy 61 TGTGATTTGCCCTGGATGCATGATGTTCCACTGGGTGATGAAGTATATTCAGAAATT 120
Db 871 TGTGATTTGCCCTGGATGCATGATGTTCCACTGGGTGATGAAGTATATTCAGAAATT 930
Qy 121 CCTCAGCCCTCTTTTATCAACTCTGAATATTTTCCAATATCTCTGCTTAATATCAATAA 180
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Qy 181 ATGAAAAATGCTACTACCTGTATAAGAAAGAAAGATGATTACATCAGGGGTTTCAGTC 240
Db 991 ATGAAAAATGCTACTACCTGTATAAGAAAGAAAGATGATTACATCAGGGGTTTCAGTC 1050
Qy 241 CACAGAAATTTGCTGATCTCACTTTTGCAACTGGCAAAATAATTTGGACATGCTCAAA 300
Db 1051 CACAGAAATTTGCTGATCTCACTTTTGCAACTGGCAAAATAATTTGGACATGCTCAAA 1110
Qy 301 TTAAGGAGACATAGATTTCAGATTCAGATTCATTAGCAAAAGCTTCATTAGCA 360
Db 1111 TTAAGGAGACATAGATTTCAGATTCAGATTCATTAGCAAAAGCTTCATTAGCA 1170
Qy 361 TTCTTACAAAAGCAATTAGGACTTCATTAAGATTTTGATCATGTTGGAGCTGCTGATTGAA 420
Db 1171 TTCTTACAAAAGCAATTAGGACTTCATTAAGATTTTGATCATGTTGGAGCTGCTGATTGAA 1230
Qy 421 GGAGATGATGAGATCTTTATTTCCAGGGACCAACATTTAAACACAAACCAATCAACATCATG 480
Db 1231 GGAGATGATGAGATCTTTATTTCCAGGGACCAACATTTAAACACAAACCAATCAACATCATG 1290
Qy 481 TTACAGAACTCTTCAGGAATAGAAATACAAATT 514
Db 1291 TTACAGAACTCTTCAGGAATAGAAATACAAATT 1324
RESULT 7
CR608325 1562 bp mRNA linear HTC 21-JUL-2004
LOCUS
DEFINITION CR608325 full-length cDNA clone CSODI067YM18 of Placenta Cot 25-normalized
of Homo sapiens (human).

CR608325
CR608325.1 GI:50489132
HTC; CNSLT_CDNA.
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 1562)
Li,W.B., Gruber,C., Jesse,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Paradise Avenue
2 (bases 1 to 1562)
Genoscope.
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequençage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
Location/Qualifiers
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/db_xref="taxon:9606"
/clone="CSODI067YM18"
/tissue_type="Placenta Cot 25-normalized"
/plasmid="pCMVSPORT_6"
ORIGIN
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Best Local Similarity 99.8%; Pred. No. 4.6e-121;
Matches 505; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GGACATCTTTTGGTGAGCAACGGTTATTAGAGTCTTAGTGAAGATTCAGATTTCAGA 60
Db 1057 GGACATCTTTTGGTGAGCAACGGTTATTAGAGTCTTAGTGAAGATTCAGATTTCAGA 1116
Qy 61 TGTGATTTGCCCTGGATGCATGATGTTCCACTGGGTGATGAAGTATATTCAGAAATT 120
Db 1117 TGTGATTTGCCCTGGATGCATGATGTTCCACTGGGTGATGAAGTATATTCAGAAATT 1176
Qy 121 CCTCAGCCCTCTTTTATCAACTCTGAATATTTTCCAATATCTCTGCTTAATATCAATAA 180
Db 1177 CCTCAGCCCTCTTTTATCAACTCTGAATATTTTCCAATATCTCTGCTTAATATCAATAA 1236
Qy 181 ATGAAAAATGCTACTACCTGTATAAGAAAGAAAGATGATTACATCAGGGGTTTCAGTC 240
Db 1237 ATGAAAAATGCTACTACCTGTATAAGAAAGAAAGATGATTACATCAGGGGTTTCAGTC 1296
Qy 241 CACAGAAATTTGCTGATCTCACTTTTGCAACTGGCAAAATAATTTGGACATGCTCAAA 300
Db 1297 CACAGAAATTTGCTGATCTCACTTTTGCAACTGGCAAAATAATTTGGACATGCTCAAA 1356
Qy 301 TTAAGGAGACATAGATTTCAGATTCAGATTCATTAGCAAAAGCTTCATTAGCA 360
Db 1357 TTAAGGAGACATAGATTTCAGATTCAGATTCATTAGCAAAAGCTTCATTAGCA 1416
Qy 361 TTCTTACAAAAGCAATTAGGACTTCATTAAGATTTTGATCATGTTGGAGCTGCTGATTGAA 420
Db 1417 TTCTTACAAAAGCAATTAGGACTTCATTAAGATTTTGATCATGTTGGAGCTGCTGATTGAA 1476
Qy 421 GGAGATGATGAGATCTTTATTTCCAGGGACCAACATTTAAACACAAACCAATCAACATCATG 480
Db 1477 GGAGATGATGAGATCTTTATTTCCAGGGACCAACATTTAAACACAAACCAATCAACATCATG 1536
Qy 481 TTACAGAACTCTTCAGGAATAGAA 506
|||||

Db 1537 TTACGAACTCTTCAGGAATAGAGAA 1562

RESULT 8
BC025674

LOCUS DEFINITION BC025674 1793 bp mRNA linear HTC 12-OCT-2004
Homo sapiens cDNA clone IMAGE:5203018, containing frame-shift errors.

ACCESSION BC025674
VERSION BC025674.1 GI:19343677

KEYWORDS HTC.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE
AUTHORS

1 (bases 1 to 1793)
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buettow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Uedin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, K.D., Mullany, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D., Dickinson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butlerfield, Y.S., Krzywicki, M.I., Skalska, U., Smalick, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

1247932

2 (bases 1 to 1793)
Director MGC Project.
Direct Submission

Submitted (06-MAR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgapbe@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),
Gaithersburg, Maryland.
Web site: <http://www.nisc.nih.gov/>
Contact: nisc_mgc@nhgri.nih.gov

Akhter, N., Ayale, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Hachighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R., Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W., Turgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at: <http://image.llnl.gov>
Series: IRAC Plate: 49 Row: e Column: 9
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 31543409
This clone has the following problem: frame shifted.

FEATURES
source
Location/Qualifiers
1. .1793

ORGANISM
Query Match 97.9%; Score 503; DB 3; Length 1793;
Best Local Similarity 99.8%; Pred. No. 1.1e-120;
Matches 514; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 GGACATTTCTTTGGTGGAGCAACGGTTATTTCAGACTCTTAGTGAAGATTCAGAGATTTCAGA 60
Db 1008 GGACATTTCTTTGGTGGAGCAACGGTTATTTCAGACTCTTAGTGAAGATTCAGAGATTTCAGA 1067

QY 61 TGTGTTATTCCTCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120
Db 1068 TGTGTTATTCCTCGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1127

QY 121 CCTCAGCCCTC-TTTTTATCAACTCTGAAATATTTCCAATATCTCTGCTAATATCAATAA 179
Db 1128 CCTCAGCCCTC-TTTTTATCAACTCTGAAATATTTCCAATATCTCTGCTAATATCAATAA 1187

QY 180 AATGAAAAAATGCTACTCACTGATTAAGAAAGAAAGATGATTTACAAATCAGGGGTTTCAGT 239
Db 1188 AATGAAAAAATGCTACTCACTGATTAAGAAAGAAAGATGATTTACAAATCAGGGGTTTCAGT 1247

QY 240 CCACAGAAATTTGCTGACTTCACTTTTGCACATGCGCAAAATTAATGGACACATGCTCAA 299
Db 1248 CCACAGAAATTTGCTGACTTCACTTTTGCACATGCGCAAAATTAATGGACACATGCTCAA 1307

QY 300 ATTAAAGGGAGACATAGATTTCAATGCGAGCTATTGATCTTAGCAACAAAGCTTCATAGC 359
Db 1308 ATTAAAGGGAGACATAGATTTCAATGCGAGCTATTGATCTTAGCAACAAAGCTTCATAGC 1367

QY 360 ATTCTTACAAAAGCATTTAGGACTTCAATAAGATTTTGTAGTCAGTGGGACTGCTTGATTGA 419
Db 1368 ATTCTTACAAAAGCATTTAGGACTTCAATAAGATTTTGTAGTCAGTGGGACTGCTTGATTGA 1427

QY 420 AGGAGATGATGAGAATCTTTATTCAGGAGCAACATTAACCAACCAATCAACACATCAT 479
Db 1428 AGGAGATGATGAGAATCTTTATTCAGGAGCAACATTAACCAACCAATCAACACATCAT 1487

QY 480 GTTACAGAACTCTTCAGGATAGAGAAATCAATTT 514
Db 1488 GTTACAGAACTCTTCAGGATAGAGAAATCAATTT 1522

RESULT 9
CR615354

LOCUS DEFINITION CR615354 1531 bp mRNA linear HTC 21-JUL-2004
full-length cDNA clone CS0D1049YE02 of Placenta Cot 25-normalized of Homo sapiens (human).

ACCESSION CR615354
VERSION CR615354.1 GI:50496161

KEYWORDS HTC; CNSIT_cDNA.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL : <http://fulllength.invitrogen.com/> Invitrogen Corporation 1600 Faraday Avenue
2 (bases 1 to 1531)
Genoscope.
Direct Submission

JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)

COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.

FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clones="CSODI049YE02"
/tissue_type="Placenta Cot 25-normalized"
/plasmid="pCMVSPORT_6"

ORIGIN
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Matches 500; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GGACATCTTTTGGTGGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAGATTTCAGA 60
Db 1031 GGACATCTTTTGGTGGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAGATTTCAGA 1090
Qy 61 TGTGGTATGTCCTGGATGCATGATGTTTCCACTGGGTGATGAAGTATATTCAGAAATT 120
Db 1091 TGTGGTATGTCCTGGATGCATGATGTTTCCACTGGGTGATGAAGTATATTCAGAAATT 1150
Qy 121 CCTCAGCCCTCTTTTATCACTCTCAATATTTCCAAATATCTCGCTAAATATCATATAA 180
Db 1151 CCTCAGCCCTCTTTTATCACTCTCAATATTTCCAAATATCTCGCTAAATATCATATAA 1210
Qy 181 ATGAAAAATGCTACTCACTGATAAAGAAAGAGATGATTACAAATCAGGGGTTTCAGTC 240
Db 1211 ATGAAAAATGCTACTCACTGATAAAGAAAGAGATGATTACAAATCAGGGGTTTCAGTC 1270
Qy 241 CACGAGAAATTTGCTGACTTCACTTTTGCACATGCGCAAAATAATTTGGACACATGCTCAA 300
Db 1271 CACGAGAAATTTGCTGACTTCACTTTTGCACATGCGCAAAATAATTTGGACACATGCTCAA 1330
Qy 301 TTAAGGAGACATAGATTCAAAATGACCTTATGATCTTAGCAACAAAGCTTCATTAGCA 360
Db 1331 TTAAGGAGACATAGATTCAAAATGACCTTATGATCTTAGCAACAAAGCTTCATTAGCA 1390
Qy 361 TTCTTACAAAAGCAATTTAGGACTTCATAAAGATTTTGTATCAGTGGGACTGCTTGATTGAA 420
Db 1391 TTCTTACAAAAGCAATTTAGGACTTCATAAAGATTTTGTATCAGTGGGACTGCTTGATTGAA 1450
Qy 421 GGAGATGATGAGATCTTTATTTCCAGGGACCAACATTAACACAAATCAACATCATG 480
Db 1451 GGAGATGATGAGATCTTTATTTCCAGGGACCAACATTAACACAAATCAACATCATG 1510
Qy 481 TTACAGAACTCTTCAGGAATA 501
Db 1511 TTACAGAACTCTTCAGGAATA 1531

RESULT 10
AL575852/c 1022 bp mRNA linear EST 06-APR-2004
LOCUS AL575852 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION clone CSODI067Y18 3-PRIME, mRNA sequence.
ACCESSION AL575852
VERSION AL575852.3 GI:46248763
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1022)
AUTHORS Li.W.B., Gruber,C., Jessee,J. and Polayes,D.

TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On Feb 16, 2001 this sequence version replaced gi:31314148.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
3382.r

For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?8=CSODI067BG09NP1&c=3382.r.

FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clones="CSODI067Y18"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Query Match 97.0%; Score 498.6; DB 1; Length 1022;
Best Local Similarity 98.4%; Pred. No. 1.4e-119;
Matches 498; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
Qy 1 GGACATCTTTTGGTGGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAGATTTCAGA 60
Db 506 GGACATCTTTTGGTGGAGCAACGGTTATTTCAGACTCTTAGTGAAGATCAGAGATTTCAGA 447
Qy 61 TGTGGTATGTCCTGGATGCATGATGTTTCCACTGGGTGATGAAGTATATTCAGAAATT 120
Db 446 TGTGGTATGTCCTGGATGCATGATGTTTCCACTGGGTGATGAAGTATATTCAGAAATT 387
Qy 121 CCTCAGCCCTCTTTTATCACTCTCAATATTTCCAAATATCTCGCTAAATATCATATAA 180
Db 386 CCTCAGCCCTCTCGKTTATCACTCTGAATATTTCCAAATATCTCGCTAAATATCATATAA 327
Qy 181 ATGAAAAATGCTACTCACTGATAAAGAAAGAGATGATTACAAATCAGGGGTTTCAGTC 240
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Qy 241 CACGAGAAATTTGCTGACTTCACTTTTGCACATGCGCAAAATAATTTGGACACATGCTCAA 300
Db 266 CACGAGAAATTTGCTGACTTCACTTTTGCMACTGGCAAAATAATTTGGACACATGCTCAA 207
Qy 301 TTAAGGAGACATAGATTCAAAATGACCTTATGATCTTAGCAACAAAGCTTCATTAGCA 360
Db 206 TTAAGGAGACATAGATTCAAAATGACCTTATGATCTTAGCAACAAAGCTTCATTAGCA 147
Qy 361 TTCTTACAAAAGCAATTTAGGACTTCATAAAGATTTTGTATCAGTGGGACTGCTTGATTGAA 420
Db 146 TTCTTACAAAAGCAATTTAGGACTTCATAAAGATTTTGTATCAGTGGGACTGCTTGATTGAA 87
Qy 421 GGAGATGATGAGATCTTTATTTCCAGGGACCAACATTAACACAAATCAACATCATG 480
Db 86 GGAGATGATGAGATCTTTATTTCCAGGGACCAACATTAACACAAATCAACATCATG 27
Qy 481 TTACAGAACTCTTCAGGAATAGAGAA 506
Db 26 TTACAGAACTCTTCAGGAATAGAGAA 1

RESULT 11
AW071677/c 519 bp mRNA linear EST 13-OCT-1999
LOCUS AW071677

DEFINITION w553b01.x1 NCI_CGAP Brn25 Homo sapiens cDNA clone IMAGE:2500873 3' similar to SW:PAPA HUMAN Q13093 PLATELET-ACTIVATING FACTOR ACETYLDHOLASE PRECURSOR i, mRNA sequence.

ACCESSION AW071677

VERSION AW071677.1

KEYWORDS GI:6026675

SOURCE EST.

ORGANISM Homo sapiens (human)

REFERENCE Homo sapiens Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 519)

AUTHORS NCI/NINDS-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index

JOURNAL Unpublished (1998)

COMMENT Contact: Robert Straubeberg, Ph.D.
Email: sgabbs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco
High quality sequence stop: 461.

FEATURES

Location/Qualifiers	1..519
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..db_xref="taxon:9606"	
..clone="IMAGE:2500873"	
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..clone_lib="NCI_CGAP_Brn25"	
..note="Organ: brain; Vector: pTV73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not 1; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', TGTTACCACTCGAAGTGAGCGCGGCATAGGTTTTTTTTTTTTTTTTTTTTTTT T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pTV73 vector. Library is normalized, and was constructed by Bento Soares and M.Fatima Bonaldo."	

ORIGIN

Query Match	96.8%;	Score	497.4;	DB	2;	Length	519;
Best Local Similarity	99.8%;	Pred.	No. 2.5e-119;				
Matches	498;	Conservative	0;	Mismatches	1;	Indels	0;
Gaps	0;						
QY	16	GGAGCAACCGGTATTTCAGACTCTTAGTGAAGATCCAGAGATTCAGATGTGGTATGCGCCG	75				
Db	519	GGAGCAACCGGTATTTCAGACTCTTAGTGAAGATCCAGAGATTCAGATGTGGTATGCGCCG	460				
QY	76	GATGATGATGATGTTTCCACTCGGTGATGAAGTATATTCAGAAATTCCTCAGCCCTCTTT	135				
Db	459	GATGATGATGATGTTTCCACTCGGTGATGAAGTATATTCAGAAATTCCTCAGCCCTCTTT	400				
QY	136	TTTATCAACTCTGAAATATTTTCAATATCTCTGCTTAATCATATAAATGAAAAATGCTAC	195				
Db	399	TTTATCAACTCTGAAATATTTCCAAATCTCTGCTTAATCATATAAATGAAAAATGCTAC	340				
QY	196	TCACCTGATAAAGAAAGATGATTACAAATCAGGGGTTCAGTCCACAGAAATTTGCT	255				
Db	339	TCACCTGATAAAGAAAGATGATTACAAATCAGGGGTTCAGTCCACAGAAATTTGCT	280				
QY	256	GACTTTCACCTTTGGCACTGGCAAAATAATTGACACATGCTCAAAATTAAGGAGACATA	315				
Db	279	GACTTTCACCTTTGGCACTGGCAAAATAATTGACACATGCTCAAAATTAAGGAGACATA	220				

ORIGIN		TAG_SEQ=AATCG		FEATURES		Location/Qualifiers	
Query Match		92.6%; Score 475.8; DB 2; Length 560;		Best Local Similarity 96.5%; Pred. No. 1.1e-113;		1..505	
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						/dev_stages="8-9 weeks"	
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						/clone_lib="NCI_CGAP_P13"	
						/note="Organ: Placenta; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: Ecor I; Site 2: Not I; NCI CGAP P13 is a subcloned cDNA library constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an Ecor I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tags for this library are GA, AGGA. For additional information, contact: Bento Soares, bento-soares@uiowa.edu	
						TAG_TISSUE=placenta human 8 week	
						TAG_LIB=UI-1-BC1p	
						TAG_SEQ=GA	
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Matches 467; Conservative 0; Mismatches 0; Indels 0; Gaps 0;							
Qy	48	TCAGAGATTCAGATGTGTATTTGCCCTGGATGCGATGATGTTCCACCTGGGTGATGAAGT	107				
Db	505	TCAGAGATTCAGATGTGTATTTGCCCTGGATGCGATGATGTTCCACCTGGGTGATGAAGT	446				
Qy	108	ATATTCAGAGATTCCTCAGCCCTCTTTTATCACTCTGATATTTCCATATCTCTGC	167				
Db	445	ATATTCAGAGATTCCTCAGCCCTCTTTTATCACTCTGATATTTCCATATCTCTGC	386				
Qy	168	TAATATCATATAAATGAAAAATGCTACTCACCTGTATAAAGAAAGAGATGATTAACAT	227				
Db	385	TAATATCATATAAATGAAAAATGCTACTCACCTGTATAAAGAAAGAGATGATTAACAT	326				
Qy	228	CAGGGGTTCACTCCACCAAGAAATTTTGTGACTTCACTTTTGCACCTGCAAAATTAATTGG	287				
Db	325	CAGGGGTTCACTCCACCAAGAAATTTTGTGACTTCACTTTTGCACCTGCAAAATTAATTGG	266				
Qy	288	ACACATGCTCAATTAAGGGAGACATAGATTCAATGCGCTATTGATCTTAGCAACAA	347				
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Qy	348	AGCTTCATTAGCATTTTACAAAAGCACTTAGGACTTCATAAAGATTTTGATCAGTGGGA	407				
Db	205	AGCTTCATTAGCATTTTACAAAAGCACTTAGGACTTCATAAAGATTTTGATCAGTGGGA	146				
Qy	408	CTGCTTGATTGAAGGAGATGATGAGAACTTTATTCAGGGACCAACATTAACACCAACAA	467				
Db	145	CTGCTTGATTGAAGGAGATGATGAGAACTTTATTCAGGGACCAACATTAACACCAACAA	86				
Qy	468	TCAACACATCATGTTTACAGAACTCTTTCAGGAATAGAGAAATTAACATTT	514				
Db	85	TCAACACATCATGTTTACAGAACTCTTTCAGGAATAGAGAAATTAACATTT	39				
RESULT 14							
BX330257/c							
LOCUS							
DEFINITION							
BX330257 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA							
clone CS0D1034YP21 3-PRIME, mRNA sequence.							
BX330257							
ACCESSION							
BX330257							
VERSION							
BX330257.2							
GI:46267134							

ORIGIN		TAG_SEQ=AATCG		FEATURES		Location/Qualifiers	
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						/db_xref="taxon:9606"	
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						/clone_lib="NCI_CGAP_P13"	
						/note="Organ: Placenta; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: Ecor I; Site 2: Not I; NCI CGAP P13 is a subcloned cDNA library constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an Ecor I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tags for this library are GA, AGGA. For additional information, contact: Bento Soares, bento-soares@uiowa.edu	
						TAG_TISSUE=placenta human 8 week	
						TAG_LIB=UI-1-BC1p	
						TAG_SEQ=GA	
ORIGIN		Query Match 90.9%; Score 467; DB 5; Length 505;		Best Local Similarity 100.0%; Pred. No. 2.2e-111;			
Matches 467; Conservative 0; Mismatches 0; Indels 0; Gaps 0;							
Qy	48	TCAGAGATTCAGATGTGTATTTGCCCTGGATGCGATGATGTTCCACCTGGGTGATGAAGT	107				
Db	505	TCAGAGATTCAGATGTGTATTTGCCCTGGATGCGATGATGTTCCACCTGGGTGATGAAGT	446				
Qy	108	ATATTCAGAGATTCCTCAGCCCTCTTTTATCACTCTGATATTTCCATATCTCTGC	167				
Db	445	ATATTCAGAGATTCCTCAGCCCTCTTTTATCACTCTGATATTTCCATATCTCTGC	386				
Qy	168	TAATATCATATAAATGAAAAATGCTACTCACCTGTATAAAGAAAGAGATGATTAACAT	227				
Db	385	TAATATCATATAAATGAAAAATGCTACTCACCTGTATAAAGAAAGAGATGATTAACAT	326				
Qy	228	CAGGGGTTCACTCCACCAAGAAATTTTGTGACTTCACTTTTGCACCTGCAAAATTAATTGG	287				
Db	325	CAGGGGTTCACTCCACCAAGAAATTTTGTGACTTCACTTTTGCACCTGCAAAATTAATTGG	266				
Qy	288	ACACATGCTCAATTAAGGGAGACATAGATTCAATGCGCTATTGATCTTAGCAACAA	347				
Db	265	ACACATGCTCAATTAAGGGAGACATAGATTCAATGCGCTATTGATCTTAGCAACAA	206				
Qy	348	AGCTTCATTAGCATTTTACAAAAGCACTTAGGACTTCATAAAGATTTTGATCAGTGGGA	407				
Db	205	AGCTTCATTAGCATTTTACAAAAGCACTTAGGACTTCATAAAGATTTTGATCAGTGGGA	146				
Qy	408	CTGCTTGATTGAAGGAGATGATGAGAACTTTATTCAGGGACCAACATTAACACCAACAA	467				
Db	145	CTGCTTGATTGAAGGAGATGATGAGAACTTTATTCAGGGACCAACATTAACACCAACAA	86				
Qy	468	TCAACACATCATGTTTACAGAACTCTTTCAGGAATAGAGAAATTAACATTT	514				
Db	85	TCAACACATCATGTTTACAGAACTCTTTCAGGAATAGAGAAATTAACATTT	39				
RESULT 14							
BX330257/c							
LOCUS							
DEFINITION							
BX330257 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA							
clone CS0D1034YP21 3-PRIME, mRNA sequence.							
BX330257							
ACCESSION							
BX330257							
VERSION							
BX330257.2							
GI:46267134							

ORIGIN		TAG_SEQ=AATCG		FEATURES		Location/Qualifiers	
Query Match		92.6%; Score 475.8; DB 2; Length 560;		Best Local Similarity 96.5%; Pred. No. 1.1e-113;		1..505	
Matches 497; Conservative 0; Mismatches 17; Indels 1; Gaps 1;						/organism="Homo sapiens"	
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						/dev_stage="8-9 weeks"	
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						/clone_lib="NCI CGAP P13"	
						/note="Organ: Placenta; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: Ecor I; Site 2: Not I; NCI CGAP_P13 is a subcloned cDNA library constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an Ecor I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tags for this library are GA, AGGAA. For additional information, contact: Bento Soares, bento-soares@uiowa.edu	
						TAG_TISSUE=placenta human 8 week	
						TAG_LIB=UI-1-BC1p	
						TAG_SEQ=GA	
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		Matches 467; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
Qy	48	TCAGAGATTCAGATGTGTATTTGCCCTGGATGCGATGATGTTCCACCTGGGTGATGAAGT	107				
Db	505	TCAGAGATTCAGATGTGTATTTGCCCTGGATGCGATGATGTTCCACCTGGGTGATGAAGT	446				
Qy	108	ATATTCAGAGATTCCTCAGCCCTCTTTTATCACTCTGATATTTCCATATCTCTGC	167				
Db	445	ATATTCAGAGATTCCTCAGCCCTCTTTTATCACTCTGATATTTCCATATCTCTGC	386				
Qy	168	TAATATCATATAAATGAAAAATGCTACTCACCTGTATAAAGAAAGAGATGATTAACAT	227				
Db	385	TAATATCATATAAATGAAAAATGCTACTCACCTGTATAAAGAAAGAGATGATTAACAT	326				
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Qy	288	ACACATGCTCAAAATTAAGGGAGACATAGATTCAAATGCGAGCTATTGATCTTAGCAACAA	347				
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Qy	348	AGCTTCATTAGCATTTCTTACAAAAGCACTTAGGACTTCATAAAGATTTTGATCAGTGGGA	407				
Db	205	AGCTTCATTAGCATTTCTTACAAAAGCACTTAGGACTTCATAAAGATTTTGATCAGTGGGA	146				
Qy	408	CTGCTTGATTGAAGGAGATGATGAGAACTTTATTCAGGGACCAACATTAACACCAACAA	467				
Db	145	CTGCTTGATTGAAGGAGATGATGAGAACTTTATTCAGGGACCAACATTAACACCAACAA	86				
Qy	468	TCAACACATCATGTTTACAGAACTCTTTCAGGAATAGAGAAATTAACAATTT	514				
Db	85	TCAACACATCATGTTTACAGAACTCTTTCAGGAATAGAGAAATTAACAATTT	39				
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LOCUS							
DEFINITION							
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ACCESSION							
VERSION							
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mRNA							
linear							
EST 07-APR-2004							
BX330257 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA							
clone CS0D1034YP21 3-PRIME, mRNA sequence.							
BX330257							
BX330257.2							
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KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
AUTHORS 1 (bases 1 to 818)
TITLE Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
JOURNAL Full-length cDNA libraries and normalization
COMMENT On May 1, 2003 this sequence version replaced gi:30311923.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
2019.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?sa=CS0BAK056DG02NM1&c=2019.r.
FEATURES
Location/Qualifiers
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primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized."
ORIGIN
Query Match 90.6%; Score 465.8; DB 5; Length 818;
Best Local Similarity 96.4%; Pred. No. 5.1e-111;
Matches 487; Conservative 0; Mismatches 17; Indels 1; Gaps 1;
QY 1 GGACATCTTTTGGTGAGCAACGGTATTTCAGACTCTTAGTGAAGTCAGAGATTTCAGA 60
DB 542 GGGCATCTTATGTTGGAGCAACGGTATTTCAGACTCTTAGTGAAGTCAGAGATTTCAGA 483
QY 61 TGTGGTATGCGCTGGATGCAATGGATGTTTCCACTGGGTGATGAAGTATATTCAGAAAT 120
DB 482 TGTGTAATGCCCTGGATGCAATGGATGTTTCCGCTGGGTGATGAAGTATATTCAGAAAT 423
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DB 422 CCTCAGCCCTCTTTTATCACTGATGAATATTCAGAAATATTCCTGCTAATATCAATAAA 363
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QY 301 TTAAGGAGACATAGATTCAATGCGAGCTATTGATCTTAGCAACAAAGCTTCATTAGCA 360
DB 242 TTAAGGAGACATAGATTCAATGCGAGCTATTGATCTTAGCAACAAAGCTTCATTAGCA 183
QY 361 TTCTTACAAAAGCAATTTAGGACTTCATAAAGATTTTCATCAGTGGGACTGCTGATTGAA 420
DB 182 TTCTTACAAAAGCAATTTAGGACTTCATAAAGATTTTCATCAGTGGGACTGCTGATTGAA 123
QY 421 GGAGATGATGAGATCTTATTTCCAGGACCAACATTAACACCAATCAACATCATG 480
DB 122 GGAGATGATGAGATCTTATGCGAGGACCAACATTAACACCAATCAACATCATG 64
QY 481 TTACAGAACTCTTCAGGAATAGAGA 505
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Db 63 TTACAGAACTCTCAGGAAGAGAAA 39
|||||
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LOCUS AL573565 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION Clone CS0DI049YE02 3-PRIME, mRNA sequence.
ACCESSION AL573565
VERSION AL573565.2 GI:31294910
SOURCE EST.
KEYWORDS Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
TITLE 1 (bases 1 to 946)
JOURNAL Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
COMMENT Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 15, 2001 this sequence version replaced gi:12932922.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
3382.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0DI049BC01NP1&c=3382.r.
FEATURES
Location/Qualifiers
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/notes="1st strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized."
ORIGIN
Query Match 89.3%; Score 459; DB 1; Length 946;
Best Local Similarity 92.4%; Pred. No. 3.2e-109;
Matches 463; Conservative 16; Mismatches 22; Indels 0; Gaps 0;
QY 1 GGACATCTTTTGGTGAGCAACGGTATTTCAGACTCTTAGTGAAGTCAGAGATTTCAGA 60
DB 501 GGACATCTTTTGGTGAGCAACGGTATTTCAGACTCTTAGTGAAGTCAGAGATTTCAGA 442
QY 61 TGTGGTATTCCTTCCTGGATGCAATGGATGTTTCCACTGGGTGATGAAGTATATTCAGAAAT 120
DB 441 TGTGGTATTCCTTCCTGGATGCAATGGATGTTTCCACTGGGTGATGAAGTATATTCAGAAAT 382
QY 121 CCTCAGCCCTCTTTTATCACTCTGAATATTTCAATATCTCTGCTAATATCAATAAA 180
DB 381 CCTCAGCCCTCTTTTATCACTCTGAATATTTCAATATCTCTGCTAATATCAATAAA 322
QY 181 ATGAAAAATGCTACTCACCCTGATAAAGAAAGATGATTACAATCAGGGGTTTCAGTC 240
DB 321 ATGAAAAATGCTACTCACCCTGATAAAGAAAGATGATTACAATCAGGGGTTTCAGTC 262
QY 241 CACAGAAATTTGCTGACTTTCACCTTTTGCAACTGGCAAAATFAATGGACACATGCTCAAA 300
DB 261 CACAGAAATTTGCTGACTTTCACCTTTTGCAACTGGCAAAATFAATGGACACATGCTCAAA 202
QY 301 TTAAGGAGACATAGATTCAATGCGAGCTATTGATCTTAGCAACAAAGCTTCATTAGCA 360
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Qy	421	GGAGATGATGAGATCTTTATCCAGGGACCAACATTTACACACCAATCAACACATCATG	480
Db	81	GGAGATGATGAGATCTTTATCCAGGGACCAACATTTAAYACAACCAATCAACACTTCWTG	22
Qy	481	TTACAGAACTCTTCAGGAATA	501
Db	21	TTACAGAACTCTTCAGGAATA	1

Search completed: March 15, 2005, 18:21:48
 Job time : 2080.29 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 15, 2005, 09:47:50 ; Search time 165.735 Seconds
(without alignments)
1029.119 Million cell updates/sec

Title: US-09-922-067F-14
Perfect score: 2358
Sequence: 1 MYPKLVLCGLAVVY.....INTNQHMLNQGSGIEKYN 441

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2358	100.0	441	3 AAB01942	AAB01942 Human low
2	2358	100.0	441	5 AAE14750	AAE14750 Human lip
3	2358	100.0	442	2 AAR64928	AAR64928 Human T-C
4	2354	99.8	441	2 AAR71913	AAR71913 Human pla
5	2354	99.8	441	2 AAW23796	AAW23796 Human pla
6	2354	99.8	441	2 AAW09808	AAW09808 Platelet-
7	2354	99.8	441	2 AAW26498	AAW26498 Human pla
8	2354	99.8	441	2 AAW38361	AAW38361 Human pla
9	2354	99.8	441	2 AAW96334	AAW96334 Human pla
10	2354	99.8	441	2 AAW73359	AAW73359 Human PAF
11	2354	99.8	441	3 AAY88301	AAY88301 Human pla
12	2354	99.8	441	3 AAY50735	AAY50735 Human PAF
13	2354	99.8	441	3 AAB07774	AAB07774 Plasma pl
14	2354	99.8	441	4 AAE00761	AAE00761 Human pla
15	2354	99.8	441	4 AAB49451	AAB49451 Platelet-
16	2354	99.8	441	4 AAE15507	AAE15507 Human pla
17	2354	99.8	441	5 ABG61862	ABG61862 Prostate
18	2354	99.8	441	6 ABP55072	ABP55072 Human lip
19	2354	99.8	441	6 ADA19491	ADA19491 Human pla
20	2354	99.8	441	7 ADP65141	ADP65141 Human pho
21	2354	99.8	441	8 ADJ57408	ADJ57408 Human pho
22	2354	99.8	441	8 ADP12938	ADP12938 Protein e
23	2354	99.8	441	8 ADR14277	ADR14277 Human NF-
24	2354	99.8	441	8 ADR51543	ADR51543 Human lip
25	2354	99.8	441	8 ADP54611	ADP54611 Human PRO

26	2354	99.8	441	8 ADP23967	ADP23967 PRO polyp
27	2351	99.7	441	2 AAR71920	AAR71920 Human ace
28	2351	99.7	441	2 AAR71921	AAR71921 Human ace
29	2351	99.7	441	4 AAE00768	AAE00768 Human pla
30	2351	99.7	441	4 AAE00769	AAE00769 Human pla
31	2351	99.7	441	4 AAE15515	AAE15515 Human pla
32	2351	99.7	441	4 AAE15516	AAE15516 Human pla
33	2349	99.6	441	4 AAE00771	AAE00771 Human pla
34	2349	99.6	441	4 AAE15518	AAE15518 Human pla
35	2346	99.5	441	2 AAR71923	AAR71923 Human ace
36	2346	99.5	441	2 AAR71922	AAR71922 Human ace
37	2346	99.5	441	4 AAE00770	AAE00770 Human pla
38	2346	99.5	441	4 AAE00773	AAE00773 Human pla
39	2346	99.5	441	4 AAE00774	AAE00774 Human pla
40	2346	99.5	441	4 AAE00772	AAE00772 Human pla
41	2346	99.5	441	4 AAE15519	AAE15519 Human pla
42	2346	99.5	441	4 AAE15517	AAE15517 Human pla
43	2346	99.5	441	4 AAE15520	AAE15520 Human pla
44	2346	99.5	441	4 AAE15521	AAE15521 Human pla
45	2344	99.4	441	2 AAR71924	AAR71924 Human ace

ALIGNMENTS

RESULT 1
AAB01942
ID AAB01942 standard; protein; 441 AA.
XX AC AAB01942;
XX AC AAB01942;
DT 18-SEP-2000 (first entry)
XX DE Human low density lipoprotein-associated phospholipase A2 (LDL-PLA2).
XX KW Human; low density lipoprotein associated phospholipase A2; LDL-PLA2;
KW plasma PAF acetyl hydroxylase; recombinant; purification;
KW short chain phospholipid; serine-dependant phospholipase; inflammation;
KW proinflammatory; anti inflammatory; drug screening; antibody; diagnosis.
XX OS Homo sapiens.
XX WO200024910-A1.
XX PD 04-MAY-2000.
XX PF 27-OCT-1999; 99WO-GB003551.
XX PR 28-OCT-1998; 98GB-00023647.
XX PR 28-OCT-1998; 98GB-00023648.
(SMIK) SMITHKLINE BEECHAM PLC.
PI Boyd H, Tew DG;
XX WPI; 2000-350749/30.
DR N-PSDB; AAA52357.
XX Recombinant low density lipoprotein associated phospholipase A2, used to
PT produce antibodies for diagnostics, is purified using a Blue Sepharose
PT and Q Sepharose column.
XX Claim 6b; Page 17; 28pp; English.
XX The present sequence represents human LDL-PLA2. The invention relates to
CC a method for purifying recombinant low density lipoprotein-associated
CC phospholipase A2 (LDL-PLA2). The method comprises applying a cell
CC extract, supernatant or solution containing the recombinantly expressed
CC LDL-PLA2 to a zinc chelating column, applying the eluate to a Blue
CC Sepharose column, and applying that eluate to a Q Sepharose column. The
CC invention also provides a process which additionally comprises the prior
CC steps of constructing a vector comprising a cDNA encoding a histidine
CC tagged LDL-PLA2 or fragment thereof, expressing the tagged protein in a

AA64928 standard; protein; 442 AA.
AA64928;
25-MAR-2003 (revised)
18-AUG-1995 (first entry)
Human T-cell lymphoma lipoprotein-associated phospholipase-A2.
T-cell; T-lymphocyte; lipoprotein-associated phospholipase-A2; enzyme;
atherosclerosis; diagnosis; therapy; antiarteriosclerotic.
Homo sapiens.
Key Location/Qualifiers
Peptide 25..31
/note= "Peptide 4"
Peptide 115..133
/note= "Peptide 3"
Peptide 298..327
/note= "Peptide 2"
Peptide 368..393
/note= "Peptide 1"
W09500649-A1.
05-JAN-1995.
24-JUN-1994; 94WO-GB001374.
25-JUN-1993; 93GB-00013144.
11-JAN-1994; 94GB-00000413.
(SMIK) SMITHLINE BEECHAM PLC.
Macphes CH, Tew DG, Southan CD, Hickey DMB, Gloger IS;
Lawrence GMP, Rice SQ;
WPI; 1995-052086/07.
N-PSDB; AAQ81780.
Purified lipoprotein associated phospholipase A2 - used to develop prods.
for diagnosis and therapy, partic. inhibitors for treatment of
atherosclerosis.
Claim 8; Page 19; 29pp; English.
This sequence encodes an enzyme which may be used in a method of
screening compounds to identify those compounds which inhibit Lp-PLA2
which involves contacting isolated Lp-PLA2 with a test compound and
measuring the rate of turnover of an enzyme substrate as compared with
the rate of turnover in the absence of the test compound. (Updated on 25-
MAR-2003 to correct PN field.)
Sequence 442 AA;
Query Match 100.0%; Score 2358; DB 2; Length 442;
Best Local Similarity 100.0%; Pred. No. 4.5e-218;
Matches 441; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MVPKHLVFLCGLCLAVVYFDQYINPVVHMKSSAWNKKIQLVMAASFGQTKIPRGN 60
Db 1 MVPKHLVFLCGLCLAVVYFDQYINPVVHMKSSAWNKKIQLVMAASFGQTKIPRGN 60
Qy 61 GPYSVGCTDLNFDHNTKGTFLRLYYPSQDNDRLDTLIPNKEYFWGLSKFLGTHLMGNI 120
Db 61 GPYSVGCTDLNFDHNTKGTFLRLYYPSQDNDRLDTLIPNKEYFWGLSKFLGTHLMGNI 120
Qy 121 LRLFLGSMTPPANWNSPLRPGKPYPLVVFVSHGLGAFRTLYSAIGIDLASHGFIVAAVEHR 180
Db 121 LRLFLGSMTPPANWNSPLRPGKPYPLVVFVSHGLGAFRTLYSAIGIDLASHGFIVAAVEHR 180
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181 DRASATYYPKQSAAEIGDKSWLYLRTLKQEEETHIRNEQVRORAKECSQALSILIDID 240
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241 HGKPVKNALDKFDMEQKDSIDREKIAVIGHSGFGATVIQTLSQDQFRGCIADAMWF 300
301 PLGDEVYSRIPOQLFFINSEYFQYPANIIKKKCYSPDKERKMITIRGSHVONFADTFPA 360
301 PLGDEVYSRIPOQLFFINSEYFQYPANIIKKKCYSPDKERKMITIRGSHVONFADTFPA 360
361 TGIIGHMLKLGKIDISNAIDLSNKLAFLOKHLGLHKDFDOWDCLIEGDDENLIPGT 420
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421 NINTTNOHMLQNSGGIEKYN 441
421 NINTTNOHMLQNSGGIEKYN 441
RESULT 4
AA64928 standard; protein; 441 AA.
XX AC AAR71913;
XX AC AAR71913;
XX DT 25-MAR-2003 (revised)
XX DT 05-DEC-1995 (first entry)
XX DE Human plasma platelet activating factor, acetyl hydrolase (PAP-AH).
XX KW Acetyl hydrolase; AH; platelet activating factor; PAP; inflammatory;
XX KW disease; pleurisy; diagnosis.
XX OS Homo sapiens.
XX PN W09509921-A1.
XX PD 13-APR-1995.
XX PF 06-OCT-1994; 94WO-US011340.
XX PR 06-OCT-1993; 93US-00133803.
XX PA (ICOS-) ICOS CORP.
XX PI Cousens LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;
XX PI Wilder CL;
XX DR WPI; 1995-155262/20.
XX DR N-PSDB; AAQ87947.
XX PT New nucleic acid encoding platelet activating factor, acetyl hydrolase -
XX PT useful in diagnosis and for treating inflammatory diseases, e.g.
XX PT pleurisy.
XX Claim 5; Page 53-54; 88pp; English.
XX The human acetyl hydrolase gene (AAQ87947) has been isolated and
XX purified. The platelet activating factor acetyl hydrolase (AAR71913) is
XX useful in the treatment of inflammatory diseases, in particular pleurisy,
XX asthma, rhinitis and eczema. The gene may also be used in raising
XX monoclonal antibodies specific for PAP-AH that are useful in the
XX diagnosis of such diseases. (Updated on 25-MAR-2003 to correct PN field.)
XX Sequence 441 AA;
Query Match 99.8%; Score 2354; DB 2; Length 441;
Best Local Similarity 99.8%; Pred. No. 1.1e-217;
Matches 440; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MVPKHLVFLCGLCLAVVYFDQYINPVVHMKSSAWNKKIQLVMAASFGQTKIPRGN 60

Db 1 MPPKLVFLCLGCLAVVYPPDQWYINPVAHMKSSAWNKIQVLMASFGQTKIPRGN 60
 Qy 61 GPYSVGCTDLMFDTHTNKGTLRLYYPQDNDRLDTLWIPNKEYFWGLSKFLGTHWLMGNI 120
 Db 61 GPYSVGCTDLMFDTHTNKGTLRLYYPQDNDRLDTLWIPNKEYFWGLSKFLGTHWLMGNI 120
 Qy 121 LRLFGSMTPANWNSPLRPGKYPVLFVSHGLGAFRTLYSAIGIDLASHGFVAAVEHR 180
 Db 121 LRLFGSMTPANWNSPLRPGKYPVLFVSHGLGAFRTLYSAIGIDLASHGFVAAVEHR 180
 Qy 181 DRSATATYFKDQSAAEIGDKSWLYLRLTKQEBETHIRNEQVRORAKESQALSLLIID 240
 Db 181 DRSATATYFKDQSAAEIGDKSWLYLRLTKQEBETHIRNEQVRORAKESQALSLLIID 240
 Qy 241 HGKPVKNALDLKFDMEQLKDSIDREKIAVIGHSGFGATVIQTLSEDFRCGIALDAWMF 300
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 Db 301 PLGDEVYSRIPQPLFFINSEYFOYPANIIKMKKCYSPDKERKMITIRGSHVQNFADTFPA 360
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 Db 361 TGKIIIGHMLKLGKIDSNVAIDLNSKASLAFLOKHLGLHKDFQDQDCLIEGDDENLIPGT 420
 Qy 421 NINTNQHIMLQNSSGIEKYN 441
 Db 421 NINTNQHIMLQNSSGIEKYN 441

RESULT 5
 AAW23796
 ID AAW23796 standard; protein; 441 AA.

XX AC AAW23796;
 XX 25-MAR-2003 (revised)
 DT 04-NOV-1997 (first entry)
 XX
 DE Human plasma platelet activating factor acetylhydrolase.
 XX Human PAF-AH; asthma; anaphylaxis; shock; anti-inflammatory;
 KW pro-inflammatory arachidonic acid metabolite; reperfusion injury;
 KW central nervous system shock; arthritis; Crohn's disease;
 KW systemic lupus erythematosus; adult respiratory distress syndrome.
 XX
 OS Homo sapiens.
 XX US5641669-A.
 XX 24-JUN-1997.
 XX 06-OCT-1994; 94US-00318905.
 XX 06-OCT-1993; 93US-00133803.
 XX (ICOS-) ICOS CORP.
 XX Tjoelker LW, Trong HL, Cousens LS, Wilder CL, Eberhardt CD,
 PI Gray P;
 XX WPI; 1997-340947/31.
 DR N-PSDB; AAT80564.
 XX New human plasma platelet activating factor acetylhydrolase - useful as
 PT anti-inflammatory for treatment of asthma, anaphylaxis, shock, etc.
 XX Claim 1; Col 35-38; 43pp; English.
 XX The present sequence represents the purified and isolated human plasma
 CC platelet activating factor acetylhydrolase (PAF-AH). This novel
 CC polypeptide inactivates PAF and oxidatively fragmented phospholipids such

CC as pro-inflammatory arachidonic acid metabolites, and so can be used to
 CC treat inflammation by augmenting endogenous activity. Typical
 CC applications are in asthma, anaphylaxis, shock, reperfusion injury,
 CC central nervous system shock, arthritis, Crohn's disease, systemic lupus
 CC erythematosus, adult respiratory distress syndrome. The polypeptide can
 CC also be used to raise specific antibodies (Ab) which are useful as
 CC immunoassay reagents and for generating anti-idiotypic antibodies. The
 CC nucleic acid encoding the protein can be used to screen for related genes
 CC ; in hybridisation assays to assess the protein-producing cells; to
 CC generate knockout mice; to detect genetic mutations and (antisense
 CC sequences) to inhibit the protein expression. Unlike PAF receptor
 CC antagonists, the protein is a natural component of plasma. (Updated on 25
 CC -MAR-2003 to correct Pf field.)
 XX
 SQ Sequence 441 AA;

Query Match 99.8%; Score 2354; DB 2; Length 441;
 Best Local Similarity 99.8%; Pred. No. 1.1e-217;
 Matches 440; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 MPPKLVFLCLGCLAVVYPPDQWYINPVAHMKSSAWNKIQVLMASFGQTKIPRGN 60
 Db 1 MPPKLVFLCLGCLAVVYPPDQWYINPVAHMKSSAWNKIQVLMASFGQTKIPRGN 60
 Qy 61 GPYSVGCTDLMFDTHTNKGTLRLYYPQDNDRLDTLWIPNKEYFWGLSKFLGTHWLMGNI 120
 Db 61 GPYSVGCTDLMFDTHTNKGTLRLYYPQDNDRLDTLWIPNKEYFWGLSKFLGTHWLMGNI 120
 Qy 121 LRLFGSMTPANWNSPLRPGKYPVLFVSHGLGAFRTLYSAIGIDLASHGFVAAVEHR 180
 Db 121 LRLFGSMTPANWNSPLRPGKYPVLFVSHGLGAFRTLYSAIGIDLASHGFVAAVEHR 180
 Qy 181 DRSATATYFKDQSAAEIGDKSWLYLRLTKQEBETHIRNEQVRORAKESQALSLLIID 240
 Db 181 DRSATATYFKDQSAAEIGDKSWLYLRLTKQEBETHIRNEQVRORAKESQALSLLIID 240
 Qy 241 HGKPVKNALDLKFDMEQLKDSIDREKIAVIGHSGFGATVIQTLSEDFRCGIALDAWMF 300
 Db 241 HGKPVKNALDLKFDMEQLKDSIDREKIAVIGHSGFGATVIQTLSEDFRCGIALDAWMF 300
 Qy 301 PLGDEVYSRIPQPLFFINSEYFOYPANIIKMKKCYSPDKERKMITIRGSHVQNFADTFPA 360
 Db 301 PLGDEVYSRIPQPLFFINSEYFOYPANIIKMKKCYSPDKERKMITIRGSHVQNFADTFPA 360
 Qy 361 TGKIIIGHMLKLGKIDSNVAIDLNSKASLAFLOKHLGLHKDFQDQDCLIEGDDENLIPGT 420
 Db 361 TGKIIIGHMLKLGKIDSNVAIDLNSKASLAFLOKHLGLHKDFQDQDCLIEGDDENLIPGT 420
 Qy 421 NINTNQHIMLQNSSGIEKYN 441
 Db 421 NINTNQHIMLQNSSGIEKYN 441

RESULT 6
 AAW09808
 ID AAW09808 standard; protein; 441 AA.

XX AC AAW09808;
 XX 25-MAR-2003 (revised)
 DT 12-JUN-1997 (first entry)
 XX
 DE Platelet-activating factor acetylhydrolase.
 XX Human platelet-activating factor acetylhydrolase; PAF-AH; detection;
 KW mutation; V279F; substitution; restriction fragment length polymorphism;
 KW analysis; diagnosis; inherited; deficiency; severe respiratory symptom;
 KW asthmatic children; treat; inflammatory condition.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1. .41

```

FT /label= signal peptide
FT /note= "possibly contains additional peptide that is
FT cleaved to yield the mature functional enzyme"
FT 42..441
FT Protein
FT
FT /label= mature_enzyme
FT 271..275
FT /note= "contains active site serine; conforms to
FT consensus motif for mammalian and microbial lipases and
FT serine proteases"
FT
FT XX
FT XX
PN US5605801-A.
XX
XX 25-FEB-1997.
XX
XX 07-JUN-1995; 95US-00478465.
XX
XX 06-OCT-1993; 93US-00133803.
XX 06-OCT-1994; 94US-00318905.
XX
XX (ICOS-) ICOS CORP.
XX
XX Gray P, Tjoelker LW, Trong HL, Cousens LS, Wilder CL;
XX Eberhardt CD;
XX
XX WPI; 1997-153573/14.
XX N-PSDB; AAT63701.
XX
XX Detection of platelet-activating factor acetylhydrolase gene mutation -
XX by restriction length polymorphism analysis.
XX
XX Example 3; Col 33-38; 43pp; English.
XX
XX This sequence is that of human platelet-activating factor acetyl-
XX hydrolase (PAF-AH). The claimed method of the invention detects a
XX mutation (which results in a V279G substitution) in the PAF-AH gene, and
XX comprises performing a restriction fragment length polymorphism analysis
XX and differentiating between wild-type and mutant alleles on the basis of
XX the number of restriction sites. The method is useful for diagnosis of
XX inherited PAF-AH deficiency, which has been correlated with severe
XX respiratory symptoms in asthmatic children. Recombinant PAF-AH can be
XX used to treat inflammatory conditions. (Updated on 25-MAR-2003 to correct
XX PF field.)
XX
XX SQ Sequence 441 AA;
XX
XX Query Match 99.8%; Score 2354; DB 2; Length 441;
XX Best Local Similarity 99.8%; Pred. No. 1.1e-217;
XX Matches 440; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
Qy 1 MVPKPLHVLFCGCLAVVYFDFWQYINPVAHMKSSAWNKKIQLVMAAASFGQTKIPRGN 60
Db 1 MVPKPLHVLFCGCLAVVYFDFWQYINPVAHMKSSAWNKKIQLVMAAASFGQTKIPRGN 60
Qy 61 GPYSVGCTDLMFDTHTNKGTLRLYPSQDNDRLDTLWIPNKEYFWGLSKFLGTHWLMGNI 120
Db 61 GPYSVGCTDLMFDTHTNKGTLRLYPSQDNDRLDTLWIPNKEYFWGLSKFLGTHWLMGNI 120
Qy 121 LRLFLGSMTPPANWNSPLRPGCKPLVVFVSHGLGAFRTLYSAIGIDLASHGFIIVAAVEHR 180
Db 121 LRLFLGSMTPPANWNSPLRPGCKPLVVFVSHGLGAFRTLYSAIGIDLASHGFIIVAAVEHR 180
Qy 181 DRSASATYFKDQSAAEIGDKSWLYLRTLKQEEETHIRNEQVRQRAKESQALSILIDID 240
Db 181 DRSASATYFKDQSAAEIGDKSWLYLRTLKQEEETHIRNEQVRQRAKESQALSILIDID 240
Qy 241 HGKVKVNALDKPDMEQKDSIDREKTAIVGHSGGATVIQTLSEDQRFRCGIALDAWVF 300
Db 241 HGKVKVNALDKPDMEQKDSIDREKTAIVGHSGGATVIQTLSEDQRFRCGIALDAWVF 300
Qy 301 PLGDEVYSRIPOPLFFINSEYFQYPANIIKMKCYSPDKERKMITIRGSHVONFADPTFA 360
Db 301 PLGDEVYSRIPOPLFFINSEYFQYPANIIKMKCYSPDKERKMITIRGSHVONFADPTFA 360

```

/label= signal peptide
/note= "possibly contains additional peptide that is cleaved to yield the mature functional enzyme"
42..441
Protein

/label= mature_enzyme
271..275
/note= "contains active site serine; conforms to consensus motif for mammalian and microbial lipases and serine proteases"

US5605801-A.
25-FEB-1997.
07-JUN-1995; 95US-00478465.
06-OCT-1993; 93US-00133803.
06-OCT-1994; 94US-00318905.
(ICOS-) ICOS CORP.
Gray P, Tjoelker LW, Trong HL, Cousens LS, Wilder CL;
Eberhardt CD;
WPI; 1997-153573/14.
N-PSDB; AAT63701.

Detection of platelet-activating factor acetylhydrolase gene mutation - by restriction length polymorphism analysis.

Example 3; Col 33-38; 43pp; English.

This sequence is that of human platelet-activating factor acetylhydrolase (PAF-AH). The claimed method of the invention detects a mutation (which results in a V279G substitution) in the PAF-AH gene, and comprises performing a restriction fragment length polymorphism analysis and differentiating between wild-type and mutant alleles on the basis of the number of restriction sites. The method is useful for diagnosis of inherited PAF-AH deficiency, which has been correlated with severe respiratory symptoms in asthmatic children. Recombinant PAF-AH can be used to treat inflammatory conditions. (Updated on 25-MAR-2003 to correct PF field.)

SQ Sequence 441 AA;

Query Match 99.8%; Score 2354; DB 2; Length 441;
Best Local Similarity 99.8%; Pred. No. 1.1e-217;
Matches 440; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 MVPKPLHVLFCGCLAVVYFDFWQYINPVAHMKSSAWNKKIQLVMAAASFGQTKIPRGN 60
1 MVPKPLHVLFCGCLAVVYFDFWQYINPVAHMKSSAWNKKIQLVMAAASFGQTKIPRGN 60
61 GPYSVGCTDLMFDTHTNKGTLRLYPSQDNDRLDTLWIPNKEYFWGLSKFLGTHWLMGNI 120
61 GPYSVGCTDLMFDTHTNKGTLRLYPSQDNDRLDTLWIPNKEYFWGLSKFLGTHWLMGNI 120
121 LRLFLGSMTPPANWNSPLRPGCKPLVVFVSHGLGAFRTLYSAIGIDLASHGFIIVAAVEHR 180
121 LRLFLGSMTPPANWNSPLRPGCKPLVVFVSHGLGAFRTLYSAIGIDLASHGFIIVAAVEHR 180
181 DRSASATYFKDQSAAEIGDKSWLYLRTLKQEEETHIRNEQVRQRAKESQALSILIDID 240
181 DRSASATYFKDQSAAEIGDKSWLYLRTLKQEEETHIRNEQVRQRAKESQALSILIDID 240
241 HGKVKVNALDKPDMEQKDSIDREKTAIVGHSGGATVIQTLSEDQRFRCGIALDAWVF 300
241 HGKVKVNALDKPDMEQKDSIDREKTAIVGHSGGATVIQTLSEDQRFRCGIALDAWVF 300
301 PLGDEVYSRIPOPLFFINSEYFQYPANIIKMKCYSPDKERKMITIRGSHVONFADPTFA 360
301 PLGDEVYSRIPOPLFFINSEYFQYPANIIKMKCYSPDKERKMITIRGSHVONFADPTFA 360

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Qy 361 TGKIIIGHMLKKGIDISNAIDLSNKASIAFLQKHLGLHKDFQWDCLEIGDDENLIPGT 420
Db 361 TGKIIIGHMLKKGIDISNAIDLSNKASIAFLQKHLGLHKDFQWDCLEIGDDENLIPGT 420
Qy 421 NINTTQHOHMLQNSSGIEKYN 441
Db 421 NINTTQHOHMLQNSSGIEKYN 441
RESULT 7
AAW26498
ID AAW26498 standard; protein; 441 AA.
XX AAW26498;
XX
XX 25-MAR-2003 (revised)
XX 05-JAN-1998 (first entry)
XX
XX Human platelet-activating factor acetylhydrolase.
XX
XX Platelet-activating factor acetylhydrolase; PAF-AH; human; inflammation;
XX asthma; pleurisy; necrotising enterocolitis;
XX adult respiratory distress syndrome; therapy.
XX
XX Homo sapiens.
XX
XX US5656431-A.
XX
XX 12-AUG-1997.
XX
XX 07-JUN-1995; 95US-00483232.
XX
XX 06-OCT-1993; 93US-00133803.
XX 06-OCT-1994; 94US-00318905.
XX
XX (ICOS-) ICOS CORP.
XX
XX Gray P, Trong HL, Tjoelker LW, Cousens LS, Wilder CL;
XX Eberhardt CD;
XX
XX WPI; 1997-414580/38.
XX N-PSDB; AAT87048.
XX
XX Detecting lesions in human platelet-activating factor acetylhydrolase
XX gene - by comparison with defined wild-type gene sequence.
XX
XX Example 3; Col 47-50; 53pp; English.
XX
XX This polypeptide comprises human plasma platelet-activating factor
XX acetylhydrolase (PAF-AH), a protein that inactivates PAF and inactivates
XX oxidatively fragmented phospholipids such as products of the arachidonic
XX acid cascade that mediate inflammation. Its sequence was deduced from a
XX full-length cDNA clone (see AAT87048) obtained from a macrophage cDNA
XX library. Mouse, dog, cattle, chicken, rat and macaque PAF-AH polypeptides
XX (see AAW26500-505) have also been identified. Recombinant PAF-AH
XX polypeptides can be produced in prokaryotic or eukaryotic host cells and
XX used to mimic or augment normal processes of resolution of inflammation
XX in vivo. Examples describe the in vivo therapeutic effect of recombinant
XX PAF-AH products on acute inflammation, pleurisy, asthma, necrotising
XX enterocolitis and adult respiratory distress syndrome in animal models.
XX (Updated on 25-MAR-2003 to correct PF field.)
XX
XX SQ Sequence 441 AA;
XX
XX Query Match 99.8%; Score 2354; DB 2; Length 441;
XX Best Local Similarity 99.8%; Pred. No. 1.1e-217;
XX Matches 440; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
Qy 1 MVPKPLHVLFCGCLAVVYFDFWQYINPVAHMKSSAWNKKIQLVMAAASFGQTKIPRGN 60
Db 1 MVPKPLHVLFCGCLAVVYFDFWQYINPVAHMKSSAWNKKIQLVMAAASFGQTKIPRGN 60
Qy 61 GPYSVGCTDLMFDTHTNKGTLRLYPSQDNDRLDTLWIPNKEYFWGLSKFLGTHWLMGNI 120

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Db 61 GYSVGCCTDLMPDHTNKGTFRLYYPSQDNDRLDTLPNKEYFWGLSKFLGTHLWNGNI 120
 QY 121 LRLFGSMTTPANWNSPLRPEKYPVLFVSHGLGAFRTLYSAIGIDDLASHGFIVAAVEHR 180
 Db 121 LRLFGSMTTPANWNSPLRPEKYPVLFVSHGLGAFRTLYSAIGIDDLASHGFIVAAVEHR 180
 QY 181 DRSASATYFFKQDSAAEIGDKSWLYLRTLKQEEETHIRNEQVRORAKECSQALSLLDID 240
 Db 181 DRSASATYFFKQDSAAEIGDKSWLYLRTLKQEEETHIRNEQVRORAKECSQALSLLDID 240
 QY 241 HGKPVKNALDLKFDMEQLKDSIDREKIAVIGSHFGGATVIQTLSEDRFRGIALDAWMF 300
 Db 241 HGKPVKNALDLKFDMEQLKDSIDREKIAVIGSHFGGATVIQTLSEDRFRGIALDAWMF 300
 QY 301 PLGDEVYSRIPOPLFFINSEYFOYPAIIKMKKCYSPDKERKMITIRGSHVQNFADTFEA 360
 Db 301 PLGDEVYSRIPOPLFFINSEYFOYPAIIKMKKCYSPDKERKMITIRGSHVQNFADTFEA 360
 QY 361 TGKIIIGHMLKLKGDIDSNVAIDLNSKASLAFLOKHLGLHKDFDQWDCLEGGDENLIPGT 420
 Db 361 TGKIIIGHMLKLKGDIDSNVAIDLNSKASLAFLOKHLGLHKDFDQWDCLEGGDENLIPGT 420
 QY 421 NINTTNOHIMLQNSSGIEKYN 441
 Db 421 NINTTNOHIMLQNSSGIEKYN 441

RESULT 8
 ID AAW38361 standard; protein; 441 AA.
 XX AAW38361;
 AC AAW38361;
 DT 31-MAR-1998 (first entry)
 XX Human plasma platelet activating factor acetylhydrolase.
 DE Human; plasma platelet activating factor acetylhydrolase;
 KW monoclonal antibody; immunoassay; diagnosis; asthma; detection.
 XX Homo sapiens.
 OS
 XX US5698403-A.
 FN 16-DEC-1997.
 PD 07-JUN-1995; 95US-00483140.
 PF 06-OCT-1993; 93US-00133803.
 PR 06-OCT-1994; 94US-00318905.
 XX (ICOS-) ICOS CORP.
 PA Gray P, Trong HL, Tjoelker LW, Cousens LS, Wilder CL;
 PI Eberhardt CD;
 XX WPI; 1998-051484/05.
 DR N-PSDB; AAT96127.
 XX Immunoassay for platelet activating factor acetylhydrolase, PAF-AH -
 PT useful to diagnose disorders associated with abnormal PAF-AH level.
 XX Claim 1; Col 35-38; 47pp; English.

XX The present sequence was used in the development of a method for
 CC detecting human, mouse, canine, rat and monkey plasma platelet activating
 CC factor acetylhydrolases (PAF-AH). The method comprises contacting serum
 CC with PAF-AH specific monoclonal antibody (mAb) to form a PAF-AH/mAb
 CC complex, and detecting the complex. The method can be used to diagnose
 CC disorders associated with abnormal PAF-AH levels, and to monitor therapy
 CC of such disorders. Plasma PAF-AH deficiency has been correlated with
 CC severe respiratory symptoms in asthmatic children who appear to have

CC inherited the deficiency in an autosomal recessive manner
 XX SQ Sequence 441 AA;
 Query Match 99.8%; Score 2354; DB 2; Length 441;
 Best Local Similarity 99.8%; Pred. No. 1.1e-217;
 Matches 440; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MVRPKLHVLEICLGCCLAVVYFPDQVYNPVAHMKSSAWVNKIQVLMMAASFGQTKIPRGN 60
 Db 1 MVRPKLHVLEICLGCCLAVVYFPDQVYNPVAHMKSSAWVNKIQVLMMAASFGQTKIPRGN 60
 QY 61 GYSVGCCTDLMPDHTNKGTFRLYYPSQDNDRLDTLPNKEYFWGLSKFLGTHLWNGNI 120
 Db 61 GYSVGCCTDLMPDHTNKGTFRLYYPSQDNDRLDTLPNKEYFWGLSKFLGTHLWNGNI 120
 QY 121 LRLFGSMTTPANWNSPLRPEKYPVLFVSHGLGAFRTLYSAIGIDDLASHGFIVAAVEHR 180
 Db 121 LRLFGSMTTPANWNSPLRPEKYPVLFVSHGLGAFRTLYSAIGIDDLASHGFIVAAVEHR 180
 QY 181 DRSASATYFFKQDSAAEIGDKSWLYLRTLKQEEETHIRNEQVRORAKECSQALSLLDID 240
 Db 181 DRSASATYFFKQDSAAEIGDKSWLYLRTLKQEEETHIRNEQVRORAKECSQALSLLDID 240
 QY 241 HGKPVKNALDLKFDMEQLKDSIDREKIAVIGSHFGGATVIQTLSEDRFRGIALDAWMF 300
 Db 241 HGKPVKNALDLKFDMEQLKDSIDREKIAVIGSHFGGATVIQTLSEDRFRGIALDAWMF 300
 QY 301 PLGDEVYSRIPOPLFFINSEYFOYPAIIKMKKCYSPDKERKMITIRGSHVQNFADTFEA 360
 Db 301 PLGDEVYSRIPOPLFFINSEYFOYPAIIKMKKCYSPDKERKMITIRGSHVQNFADTFEA 360
 QY 361 TGKIIIGHMLKLKGDIDSNVAIDLNSKASLAFLOKHLGLHKDFDQWDCLEGGDENLIPGT 420
 Db 361 TGKIIIGHMLKLKGDIDSNVAIDLNSKASLAFLOKHLGLHKDFDQWDCLEGGDENLIPGT 420
 QY 421 NINTTNOHIMLQNSSGIEKYN 441
 Db 421 NINTTNOHIMLQNSSGIEKYN 441
 RESULT 9
 ID AAW96334 standard; protein; 441 AA.
 XX AAW96334;
 AC AAW96334;
 DT 28-JUN-1999 (first entry)
 XX Human plasma platelet-activating factor acetylhydrolase (PAF-AH).
 DE Human plasma platelet activating factor acetylhydrolase; PAF-AH; PAF;
 KW platelet activating factor; inflammation; treatment; hydrolysis;
 KW augmentation; pleurisy; asthma; rhinitis; necrotizing enterocolitis;
 KW acute respiratory distress syndrome; pancreatitis; neurological disease;
 KW HIV; human immunodeficiency virus.
 XX Homo sapiens.
 OS
 XX WO9909147-A1.
 FN 25-FEB-1999.
 PD 13-AUG-1997; 97WO-US014212.
 PF 13-AUG-1997; 97WO-US014212.
 PR 13-AUG-1997; 97WO-US014212.
 XX (ICOS-) ICOS CORP.
 PA Cousens LS, Eberhardt CD, Gray P, Trong HL, Tjoelker LW;
 PI Wilder CL;
 XX WPI; 1999-181028/15.
 DR

N-PSDB; AAX08463.

New truncated human platelet-activating factor acetylhydrolase and its encoding polynucleotides - useful for regulating inflammatory events.

Claim 1; Page 97-98; 136pp; English.

Plasma platelet-activating factor acetylhydrolase (PAF-AH) can be used to inactivate the pathological effects of PAF. Pathological conditions which can be treated include pleurisy, asthma, rhinitis, necrotizing enterocolitis, acute respiratory distress syndrome, acute pancreatitis or neurological disease associated with HIV infection. Identification and isolation of polynucleotide sequences encoding human plasma PAF-AH allows the recombinant production of PAF-AH. This makes possible the use of exogenous PAF-AH to mimic or augment normal processes of resolution of inflammation in vivo. PAF inactivation occurs by hydrolysis of the PAF sn-2 acetyl group by PAF-AH. PAF-AH also metabolises oxidatively fragmented phospholipids such as products of the arachidonic acid cascade which mediate inflammation. Administration of PAF-AH is advantageous to administering PAF receptor antagonists since PAF-AH is a product normally found in plasma. Because PAF receptor antagonists are structurally related to PAF they competitively inhibit native PAF-AH activity. Treatment with recombinant PAF-AH would augment endogenous PAF-AH activity and compensate for any inactivated endogenous enzyme

Sequence 441 AA;

XX	Platelet-activating factor acetylhydrolase; PAF-AH; human; antibody.
KW	
XX	Homo sapiens.
XX	
OS	
XX	
PN	US5847088-A.
XX	
XX	08-DEC-1998.
XX	
XX	07-JUN-1995; 95US-00485938.
PF	
XX	
XX	06-OCT-1993; 93US-00133803.
PR	
XX	06-OCT-1994; 94US-00318905.
XX	
XX	(ICOS-) ICOS CORP.
PA	
XX	
XX	Wilder CL, Tjoelker LW, Gray P, Eberhardt CD, Cousens LS;
PI	Trong HL;
PI	
XX	
XX	
DR	WPI; 1999-059148/05.
DR	N-PSDB; AAV08534.
DR	
XX	
XX	
PT	Antibodies specific for platelet-activating factor acetylhydrolase
PT	proteins - useful for detecting or purifying the proteins.
XX	
XX	
PS	Claim 1; Col 45-48; 59pp; English.

RESULT 11
AAY88301

XX	AA	AY88301 standard; protein; 441 AA.	DB	121	LRLLFGSMTPANWNSPLRPGKYPLVVFVSHGLGAFRTLYSAIGIDLASHGFIVAAVEHR	180
XX	AC	AY88301;	QY	181	DRSASATYFQDSAAABIGDKSWLYLRTLKQEBETHIRNEQVRQRAKECSQALSLLIDID	240
XX	DT	14-JUL-2000 (first entry)	DB	181	DRSASATYFQDSAAABIGDKSWLYLRTLKQEBETHIRNEQVRQRAKECSQALSLLIDID	240
XX	DE	Human platelet-activating factor acetyl hydrolase amino acid sequence.	QY	241	HGKPVKNALDLKFDMEQLKDSIDREKIAVIGHSGFGGATVIQTLSEQPRFCGIALDAWMF	300
XX	KW	Platelet-activating factor acetyl hydrolase; PAF-AH; PAF; phospholipid;	DB	241	HGKPVKNALDLKFDMEQLKDSIDREKIAVIGHSGFGGATVIQTLSEQPRFCGIALDAWMF	300
XX	KW	inflammatory response; pre-term labour; pharmaceutical composition;	QY	301	PLGDEVYSRIPOPLFFINSEYFOYPANIIKMKCYSPDKERKMITTINGSVHQNFADTFE	360
XX	KW	regulate; asthma; anaphylaxis; shock; arthritis; Crohn's disease;	DB	301	PLGDEVYSRIPOPLFFINSEYFOYPANIIKMKCYSPDKERKMITTINGSVHQNFADTFE	360
XX	KW	pancreatitis; allergic inflammation; human immunodeficiency virus; HIV.	QY	361	TGKIIGHMLKLGKIDISNAIDLSNKASLAFLOKHLGHKDFQWCLTEGDDENLPGT	420
XX	OS	Homo sapiens.	DB	361	TGKIIGHMLKLGKIDISNAIDLSNKASLAFLOKHLGHKDFQWCLTEGDDENLPGT	420
XX	FN	US6045794-A.	QY	421	NINTTNOHIMLQNSGGIEKYN 441	
XX	XX	04-APR-2000.	DB	421	NINTTNOHIMLQNSGGIEKYN 441	
XX	FF	09-JUN-1999; 99US-00328474.	QY	421	NINTTNOHIMLQNSGGIEKYN 441	
XX	PR	06-OCT-1993; 93US-00133803.	DB	421	NINTTNOHIMLQNSGGIEKYN 441	
XX	PR	06-OCT-1994; 94US-00318905.	DB	421	NINTTNOHIMLQNSGGIEKYN 441	
XX	PR	07-JUN-1995; 95US-00483232.	DB	421	NINTTNOHIMLQNSGGIEKYN 441	
XX	PR	12-AUG-1997; 97US-00910041.	DB	421	NINTTNOHIMLQNSGGIEKYN 441	
XX	PA	(ICOS-) ICOS CORP.	DB	421	NINTTNOHIMLQNSGGIEKYN 441	
XX	XX	Cousens LS, Gray P, Trong HL, Tjoelker LW, Wilder CL;	DB	421	NINTTNOHIMLQNSGGIEKYN 441	
XX	PI	Eberhardt CD;	DB	421	NINTTNOHIMLQNSGGIEKYN 441	
XX	DR	WPI; 2000-282671/24.	DB	421	NINTTNOHIMLQNSGGIEKYN 441	
XX	DR	N-PSDB; AAA10861.	DB	421	NINTTNOHIMLQNSGGIEKYN 441	
XX	XX	Treatment of mammals suffering from pre-term labor comprises	DB	421	NINTTNOHIMLQNSGGIEKYN 441	
XX	PT	administering a pharmaceutical composition comprising platelet-activating	DB	421	NINTTNOHIMLQNSGGIEKYN 441	
XX	PT	factor acetyl hydrolase enzyme.	DB	421	NINTTNOHIMLQNSGGIEKYN 441	
XX	PS	Claim 1; Col 67-70; 67pp; English.	DB	421	NINTTNOHIMLQNSGGIEKYN 441	
XX	CC	This sequence represents the human platelet-activating factor acetyl	DB	421	NINTTNOHIMLQNSGGIEKYN 441	
XX	CC	hydrolase (PAF-AH) amino acid sequence. PAF is a phospholipid and is	DB	421	NINTTNOHIMLQNSGGIEKYN 441	
XX	CC	implicated in pathological inflammatory responses (e.g. asthma,	DB	421	NINTTNOHIMLQNSGGIEKYN 441	
XX	CC	anaphylaxis, septic shock and arthritis). PAF-AH is released by	DB	421	NINTTNOHIMLQNSGGIEKYN 441	
XX	CC	hepatocytes, and macrophages and inactivates PAF. PAF-AH also inactivates	DB	421	NINTTNOHIMLQNSGGIEKYN 441	
XX	CC	oxidatively fragmented phospholipids that mediate inflammation. This	DB	421	NINTTNOHIMLQNSGGIEKYN 441	
XX	CC	sequence is specifically claimed for use in a method to treat a mammal	DB	421	NINTTNOHIMLQNSGGIEKYN 441	
XX	CC	suffering from pre-term labour. PAF-AH is included in a pharmaceutical	DB	421	NINTTNOHIMLQNSGGIEKYN 441	
XX	CC	composition which can be administered to a mammal suffering from pre-term	DB	421	NINTTNOHIMLQNSGGIEKYN 441	
XX	CC	labour. The invention relates to purified and isolated polynucleotide	DB	421	NINTTNOHIMLQNSGGIEKYN 441	
XX	CC	sequences encoding human PAF-AH and materials and methods for the	DB	421	NINTTNOHIMLQNSGGIEKYN 441	
XX	CC	recombinant production of PAF-AH products which are expected to be useful	DB	421	NINTTNOHIMLQNSGGIEKYN 441	
XX	CC	in regulating inflammatory events. The administration of PAF-AH to	DB	421	NINTTNOHIMLQNSGGIEKYN 441	
XX	CC	animals may be used for ameliorating pathological inflammatory conditions	DB	421	NINTTNOHIMLQNSGGIEKYN 441	
XX	CC	such as asthma, anaphylaxis, shock, arthritis, Crohn's disease,	DB	421	NINTTNOHIMLQNSGGIEKYN 441	
XX	CC	pancreatitis, allergic inflammation, and human immunodeficiency virus	DB	421	NINTTNOHIMLQNSGGIEKYN 441	
XX	CC	(HIV)	DB	421	NINTTNOHIMLQNSGGIEKYN 441	
XX	SQ	Sequence 441 AA;	DB	421	NINTTNOHIMLQNSGGIEKYN 441	
XX	Query Match	99.8%; Score 2354; DB 3; Length 441;	DB	421	NINTTNOHIMLQNSGGIEKYN 441	
XX	Best Local Similarity	99.8%; Pred. No. 1.1e-217;	DB	421	NINTTNOHIMLQNSGGIEKYN 441	
XX	Matches 440; Conservative	0; Mismatches 1; Indels 0; Gaps 0;	DB	421	NINTTNOHIMLQNSGGIEKYN 441	
QY	1	MVPPKHLVLCGCLAVYFPDQVYNPVAHMKSSAWNVNKKIQVMAAASFGOTKIPRGN 60	DB	1	MVPPKHLVLCGCLAVYFPDQVYNPVAHMKSSAWNVNKKIQVMAAASFGOTKIPRGN 60	
DB	1	MVPPKHLVLCGCLAVYFPDQVYNPVAHMKSSAWNVNKKIQVMAAASFGOTKIPRGN 60	DB	1	MVPPKHLVLCGCLAVYFPDQVYNPVAHMKSSAWNVNKKIQVMAAASFGOTKIPRGN 60	
QY	61	GPVSVGCTDLMPDHTNKGTFRLRYPSQDNDRLDTLWIPNKEYFWGLSKFLGTHWLMGNI 120	DB	61	GPVSVGCTDLMPDHTNKGTFRLRYPSQDNDRLDTLWIPNKEYFWGLSKFLGTHWLMGNI 120	
DB	61	GPVSVGCTDLMPDHTNKGTFRLRYPSQDNDRLDTLWIPNKEYFWGLSKFLGTHWLMGNI 120	DB	61	GPVSVGCTDLMPDHTNKGTFRLRYPSQDNDRLDTLWIPNKEYFWGLSKFLGTHWLMGNI 120	
QY	121	LRLLFGSMTPANWNSPLRPGKYPLVVFVSHGLGAFRTLYSAIGIDLASHGFIVAAVEHR 180	DB	121	LRLLFGSMTPANWNSPLRPGKYPLVVFVSHGLGAFRTLYSAIGIDLASHGFIVAAVEHR 180	

CC also have greater activity than the wild-type enzyme. This sequence
 CC represents the human PAF-AH protein which is described in the method of
 CC the invention
 XX
 SQ Sequence 441 AA;

Query Match 99.8%; Score 2354; DB 3; Length 441;
 Best Local Similarity 99.8%; Pred. No. 1.1e-217;
 Matches 440; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MPPKLVLCCLAVVYFDFQYINPVVAHMKSSAWVVKIQVLMMAASFGQTKIPRG 60
 Db 1 MPPKLVLCCLAVVYFDFQYINPVVAHMKSSAWVVKIQVLMMAASFGQTKIPRG 60

Qy 61 GPYSVGCTDLDFHNTKGTFLRLYPSQDNDRLDTLWIPNKEYFWGLSKFLGTHWLMGNI 120
 Db 61 GPYSVGCTDLDFHNTKGTFLRLYPSQDNDRLDTLWIPNKEYFWGLSKFLGTHWLMGNI 120

Qy 121 LRLFGSMTPPANWNSPLRPGKYPVVFVSHGLGAFRTLYSAIGIDLASHGFVAAVEHR 180
 Db 121 LRLFGSMTPPANWNSPLRPGKYPVVFVSHGLGAFRTLYSAIGIDLASHGFVAAVEHR 180

Qy 181 DRSATYYPKQDSAAEIGDKSWLYLRLTKQEEETHIRNEQVORAKESQALSILID 240
 Db 181 DRSATYYPKQDSAAEIGDKSWLYLRLTKQEEETHIRNEQVORAKESQALSILID 240

Qy 241 HGKPVKNALDLKFDMEQLKQSIDREKIAVIGHSGFGATVIQTLSQDFRCGIALDAMWF 300
 Db 241 HGKPVKNALDLKFDMEQLKQSIDREKIAVIGHSGFGATVIQTLSQDFRCGIALDAMWF 300

Qy 301 PLGDEVYSRIPQPLFFINSEYFOYPANIIKMKCYSPDKERKMITIRGSHVQNFADFTFA 360
 Db 301 PLGDEVYSRIPQPLFFINSEYFOYPANIIKMKCYSPDKERKMITIRGSHVQNFADFTFA 360

Qy 361 TGIIGHMLKLKGDIDSNVAIDLNSKASLAFLOKHLGLHKDFQWDCLEGGDENLIPGT 420
 Db 361 TGIIGHMLKLKGDIDSNVAIDLNSKASLAFLOKHLGLHKDFQWDCLEGGDENLIPGT 420

Qy 421 NINTNQHIMLQNSSGIEKYN 441
 Db 421 NINTNQHIMLQNSSGIEKYN 441

RESULT 13
 AAB07774
 ID AAB07774 standard; protein; 441 AA.
 XX
 AC AAB07774;
 XX
 DT 14-NOV-2000 (first entry)
 XX
 DE Plasma platelet-activating factor acetylhydrolase.
 XX
 KW Platelet-activating factor acetylhydrolase; platelet-activating factor;
 KW reperfusion injury; acute inflammation; pleurisy; asthma;
 KW necrotising enterocolitis; adult respiratory distress syndrome.
 XX
 OS Homo sapiens.
 XX
 PN US6099836-A.
 XX
 PD 08-AUG-2000.
 XX
 PF 19-JUN-1998; 98US-00100546.
 XX
 PR 06-OCT-1993; 93US-00133803.
 PR 06-OCT-1994; 94US-00318905.
 PR 07-JUN-1995; 95US-00480658.
 PR 22-JAN-1998; 98US-00010715.
 XX
 PA (ICOS-) ICOS CORP.
 XX
 PI Eberhardt CD, Gray P, Trong HL, Tjoelker LW, Wilder CL;

PI Cousens LS;
 XX WPI; 2000-531654/48.
 DR N-PSDB; AAA59579.
 XX
 PT Treating mammal susceptible to or suffering from platelet-activating
 factor mediated condition associated with reperfusion injury such as
 acute inflammation, pleurisy, asthma, necrotizing enterocolitis.
 XX
 PS Example 3; Col 49-52; 55pp; English.
 XX
 CC The specification describes a pharmaceutical composition comprising
 platelet-activating factor acetylhydrolase. The composition is
 administered for treating a mammal susceptible to or suffering from a
 platelet-activating factor-mediated condition associated with reperfusion
 injury. Diseases and conditions which may be treated include acute
 inflammation, pleurisy, asthma, necrotising enterocolitis and adult
 respiratory distress syndrome. The present sequence represents human
 plasma platelet-activating factor acetylhydrolase
 XX
 SQ Sequence 441 AA;

Query Match 99.8%; Score 2354; DB 3; Length 441;
 Best Local Similarity 99.8%; Pred. No. 1.1e-217;
 Matches 440; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MPPKLVLCCLAVVYFDFQYINPVVAHMKSSAWVVKIQVLMMAASFGQTKIPRG 60
 Db 1 MPPKLVLCCLAVVYFDFQYINPVVAHMKSSAWVVKIQVLMMAASFGQTKIPRG 60

Qy 61 GPYSVGCTDLDFHNTKGTFLRLYPSQDNDRLDTLWIPNKEYFWGLSKFLGTHWLMGNI 120
 Db 61 GPYSVGCTDLDFHNTKGTFLRLYPSQDNDRLDTLWIPNKEYFWGLSKFLGTHWLMGNI 120

Qy 121 LRLFGSMTPPANWNSPLRPGKYPVVFVSHGLGAFRTLYSAIGIDLASHGFVAAVEHR 180
 Db 121 LRLFGSMTPPANWNSPLRPGKYPVVFVSHGLGAFRTLYSAIGIDLASHGFVAAVEHR 180

Qy 181 DRSATYYPKQDSAAEIGDKSWLYLRLTKQEEETHIRNEQVORAKESQALSILID 240
 Db 181 DRSATYYPKQDSAAEIGDKSWLYLRLTKQEEETHIRNEQVORAKESQALSILID 240

Qy 241 HGKPVKNALDLKFDMEQLKQSIDREKIAVIGHSGFGATVIQTLSQDFRCGIALDAMWF 300
 Db 241 HGKPVKNALDLKFDMEQLKQSIDREKIAVIGHSGFGATVIQTLSQDFRCGIALDAMWF 300

Qy 301 PLGDEVYSRIPQPLFFINSEYFOYPANIIKMKCYSPDKERKMITIRGSHVQNFADFTFA 360
 Db 301 PLGDEVYSRIPQPLFFINSEYFOYPANIIKMKCYSPDKERKMITIRGSHVQNFADFTFA 360

Qy 361 TGIIGHMLKLKGDIDSNVAIDLNSKASLAFLOKHLGLHKDFQWDCLEGGDENLIPGT 420
 Db 361 TGIIGHMLKLKGDIDSNVAIDLNSKASLAFLOKHLGLHKDFQWDCLEGGDENLIPGT 420

Qy 421 NINTNQHIMLQNSSGIEKYN 441
 Db 421 NINTNQHIMLQNSSGIEKYN 441

RESULT 14
 AAE00761
 ID AAE00761 standard; protein; 441 AA.
 XX
 AC AAE00761;
 XX
 DT 02-JUL-2001 (first entry)
 XX
 DE Human plasma platelet-activating factor acetylhydrolase (PAF-AH).
 XX
 KW Human; platelet-activating factor acetylhydrolase; PAF-AH; arthritis;
 KW anti-inflammatory; septicemia; inflammation; haemostasis; parturition;
 KW asthma; anaphylaxis; septic shock; antibacterial.
 XX

Best Local Similarity 99.8%; Pred. No. 1.1e-217;		Matches 440; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
Qy	1	MVPPKLVFLCGLAVVYFPDMQYINPVAHMKSSAWVNKIQVLMMAASFGQTKIPRGN	60
Db	1	MVPPKLVFLCGLAVVYFPDMQYINPVAHMKSSAWVNKIQVLMMAASFGQTKIPRGN	60
Qy	61	GPYSVGCTDLMFDTNKTFLRLYYPSQDNDRLDTLWIPNKEYFWGLSKFLGTHWLMGNI	120
Db	61	GPYSVGCTDLMFDTNKTFLRLYYPSQDNDRLDTLWIPNKEYFWGLSKFLGTHWLMGNI	120
Qy	121	LRLLFGSMTPANWNSPLRPGCKYPLVVFSGHGLGAPRTLYSAIGIDLASHGFIVAAVEHR	180
Db	121	LRLLFGSMTPANWNSPLRPGCKYPLVVFSGHGLGAPRTLYSAIGIDLASHGFIVAAVEHR	180
Qy	181	DRSASATYYPKQSAABIGDKSWLYLRTLKQEEETHIRNEQVRQRAKESQALSILIDID	240
Db	181	DRSASATYYPKQSAABIGDKSWLYLRTLKQEEETHIRNEQVRQRAKESQALSILIDID	240
Qy	241	HGKEVKVALDLKFDMEQLKDSIDREKIAVIGHSGFGGATVIQTLSEDFRCGIALDAMF	300
Db	241	HGKEVKVALDLKFDMEQLKDSIDREKIAVIGHSGFGGATVIQTLSEDFRCGIALDAMF	300
Qy	301	PLGDEVYSRIPOPLFFINSEYFOYPANIIKMKCYSPDKERKMITIRGSHQNEADTFEA	360
Db	301	PLGDEVYSRIPOPLFFINSEYFOYPANIIKMKCYSPDKERKMITIRGSHQNEADTFEA	360
Qy	361	TGKIIGHMLKLKGDIDSNAAIDLSNKASLAFLOKHLGLHKDFDQWDCLEGGDDENLIPGT	420
Db	361	TGKIIGHMLKLKGDIDSNVAIDLSNKASLAFLOKHLGLHKDFDQWDCLEGGDDENLIPGT	420
Qy	421	NINTTNOHIMLQNSSGIEKYN	441
Db	421	NINTTNOHIMLQNSSGIEKYN	441

Search completed: March 15, 2005, 10:03:43
Job time : 168.735 secs

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OM protein - protein search, using sw model

Run on: March 15, 2005, 09:57:26 ; Search time 43.9559 Seconds
(without alignments)
748.938 Million cell updates/sec

Title: US-09-922-067F-14
Perfect score: 2358
Sequence: 1 MPPKLVFLCGLAVV.....INTNQHIMLQNSGIEKYN 441

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*
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2: /cgm2_6/ptodata/1/iaa/5B_COMB.pep.*
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4: /cgm2_6/ptodata/1/iaa/6B_COMB.pep.*
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6: /cgm2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2354	99.8	441	1	US-08-470-187-8
2	2354	99.8	441	1	US-08-318-905-8
3	2354	99.8	441	1	US-08-483-232-8
4	2354	99.8	441	1	US-08-483-140-8
5	2354	99.8	441	2	US-08-485-938A-8
6	2354	99.8	441	2	US-08-910-041-8
7	2354	99.8	441	3	US-09-328-474-8
8	2354	99.8	441	3	US-09-100-546-8
9	2354	99.8	441	3	US-09-010-715-8
10	2354	99.8	441	3	US-09-577-758-8
11	1964.5	83.3	444	2	US-08-485-938A-33
12	1935.5	82.1	444	1	US-08-483-140-28
13	1935.5	82.1	444	2	US-08-485-938A-32
14	1514.5	64.2	440	1	US-08-483-140-27
15	1514.5	64.2	440	2	US-08-485-938A-31
16	1131.5	48.0	422	2	US-08-485-938A-34
17	955	40.5	193	1	US-08-483-140-30
18	955	40.5	193	2	US-08-485-938A-36
19	797	33.8	392	2	US-08-886-152-3
20	797	33.8	392	3	US-09-196-222-3
21	747	31.7	392	2	US-08-886-152-1
22	747	31.7	392	3	US-09-196-222-1
23	672	28.5	171	1	US-08-483-140-29
24	672	28.5	171	2	US-08-485-938A-35
25	186	7.9	37	2	US-08-557-892-1
26	186	7.9	37	2	US-08-387-856A-1
27	186	7.9	37	3	US-09-294-384B-1

28	186	7.9	37	3	US-08-717-079-1	Sequence 1, Appli
29	170	7.2	30	2	US-08-557-892-2	Sequence 2, Appli
30	170	7.2	30	2	US-08-387-858A-2	Sequence 2, Appli
31	170	7.2	30	3	US-09-294-384B-2	Sequence 2, Appli
32	170	7.2	30	3	US-08-717-079-2	Sequence 2, Appli
33	161.5	6.8	579	4	US-09-252-991A-32124	Sequence 32124, A
34	117.5	5.0	526	4	US-08-248-796A-19924	Sequence 19924, A
35	108	4.6	622	2	US-08-664-646A-2	Sequence 2, Appli
36	108	4.6	622	2	US-09-066-285-2	Sequence 2, Appli
37	108	4.6	622	3	US-09-261-006-2	Sequence 2, Appli
38	108	4.6	622	3	US-08-951-088-2	Sequence 2, Appli
39	108	4.6	622	4	US-09-609-566-2	Sequence 2, Appli
40	108	4.6	622	4	US-09-609-570-2	Sequence 2, Appli
41	108	4.6	622	4	US-09-427-372-2	Sequence 2, Appli
42	108	4.6	622	4	US-09-693-554-2	Sequence 2, Appli
43	106.5	4.5	275	4	US-09-198-452A-181	Sequence 181, App
44	106.5	4.5	287	4	US-09-438-185A-163	Sequence 163, App
45	104	4.4	20	2	US-08-557-892-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1
US-08-470-187-8
; Sequence 8, Application US/08470187
; Patent No. 5532152
; GENERAL INFORMATION:
; APPLICANT: Cousens, Lawrence S.
; APPLICANT: Eberhardt, Christine E.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor Acetyl
; TITLE OF INVENTION: Hydrolase
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gertein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,187
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5532152and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31672
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3658
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 441 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-470-187-8

Query Match 99.8%; Score 2354; DB 1; Length 441;
Best Local Similarity 99.8%; Pred. No. 9.8e-246;

[illegible]

RESULT 2

US-08-318-905-8
 ; Sequence 8, Application US/08318905
 ; Patent No. 5641669
 ; GENERAL INFORMATION:
 ; APPLICANT: Cousins, Lawrence S.
 ; APPLICANT: Eberhardt, Christine D.
 ; APPLICANT: Gray, Patrick W.
 ; APPLICANT: Le Trong, Hai
 ; APPLICANT: Tjoelker, Larry W.
 ; APPLICANT: Wilder, Cheryl L.
 ; TITLE OF INVENTION: Platelet-Activating Factor Acetyl
 ; TITLE OF INVENTION: Hydrolase
 ; NUMBER OF SEQUENCES: 26
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Marshall, O'Toole, Gertein, Murray & Borun
 ; STREET: 6300 Sears Tower, 233 South Wacker Drive
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: USA
 ; ZIP: 60606
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/318,905
 ; FILING DATE:
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/133,803
 ; FILING DATE: 6-OCT-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: No. 5641669and, Greta E.
 ; REGISTRATION NUMBER: 35,302
 ; REFERENCE/DOCKET NUMBER: 32205
 ; TELECOMMUNICATION INFORMATION:

;; SOFTWARE: PatentIn Release #1.0, Version #1.25

;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/08/483,232

;; FILING DATE:

;; CLASSIFICATION: 435

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: US 08/318,905

;; FILING DATE: 06-OCT-1994

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: US 08/133,803

;; FILING DATE: 06-OCT-1993

;; ATTORNEY/AGENT INFORMATION:

;; NAME: No. 565643land, Greta E.

;; REGISTRATION NUMBER: 35,302

;; REFERENCE/DOCKET NUMBER: 27866/32689

;; TELEPHONE: (312) 474-6300

;; TELEFAX: (312) 474-0448

;; TELEX: 25-3658

;; INFORMATION FOR SEQ ID NO: 8:

;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 441 amino acids

;; TYPE: amino acid

;; TOPOLOGY: linear

;; MOLECULE TYPE: protein

;; US-08-483-232-8

Query Match 99.8%; Score 2354; DB 1; Length 441;

Best Local Similarity 99.8%; Pred. No. 9.8e-246;

Matches 440; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MVPKHLVFLCGLAVVPFDQYINPVAHMKSSAWVNIQVLMMAASFGQTKIPRGN 60

Db 1 MVPKHLVFLCGLAVVPFDQYINPVAHMKSSAWVNIQVLMMAASFGQTKIPRGN 60

Qy 61 GPYSVGCTDLMDFTNKGTFRLYYPSQDNDRLDTLWIPNKEYFWGLSKFLGTHWLMGNI 120

Db 61 GPYSVGCTDLMDFTNKGTFRLYYPSQDNDRLDTLWIPNKEYFWGLSKFLGTHWLMGNI 120

Qy 121 LRLFGSMTTPANNWSPLRPGKYPVVFVSHGLGAFRTLYSAIGIDLASHGFIVAAVEHR 180

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Qy 181 DRSATYYPKQSAAEIGDKSWLYLRTLKQEEETHIRNEQVORAKESQALSILID 240

Db 181 DRSATYYPKQSAAEIGDKSWLYLRTLKQEEETHIRNEQVORAKESQALSILID 240

Qy 241 HGKPVKNALDLKFMEQLKDSIDREKIAVIGHSGFGGATVIOTLSEDORFCGIALDAMWF 300

Db 241 HGKPVKNALDLKFMEQLKDSIDREKIAVIGHSGFGGATVIOTLSEDORFCGIALDAMWF 300

Qy 301 PLGDEVYSRIPQPLFFINSEYFQYIPANIIMKKKCYSPDKERKMITIRGSHVQNFADPTFA 360

Db 301 PLGDEVYSRIPQPLFFINSEYFQYIPANIIMKKKCYSPDKERKMITIRGSHVQNFADPTFA 360

Qy 361 TGKIIHMLKLGKIDSNVAIDLNSKASLAFLOKHGLHKDFDQWDCLEGGDENLIPGT 420

Db 361 TGKIIHMLKLGKIDSNVAIDLNSKASLAFLOKHGLHKDFDQWDCLEGGDENLIPGT 420

Qy 421 NINTTNOHIMLQNSSGIEKYN 441

Db 421 NINTTNOHIMLQNSSGIEKYN 441

RESULT 4

US-08-483-140-8

;; Sequence 8, Application US/08483140

;; Patent No. 5698403

;; GENERAL INFORMATION:

;; APPLICANT: ICOS Corporation

;; TITLE OF INVENTION: Platelet-Activating Factor Acetyl

;; TITLE OF INVENTION: Hydrolase

;; NUMBER OF SEQUENCES: 30

;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: Marshall, O'Toole, Gertein, Murray & Borun

;; STREET: 6300 Sears Tower, 233 South Wacker Drive

;; CITY: Chicago

;; STATE: Illinois

;; COUNTRY: USA

;; ZIP: 60606

;; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk

;; COMPUTER: IBM PC compatible

;; OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: PatentIn Release #1.0, Version #1.25

;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/08/483,140

;; FILING DATE:

;; CLASSIFICATION: 435

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: US 08/318,905

;; FILING DATE: 06-OCT-1994

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: US 08/133,803

;; FILING DATE: 06-OCT-1993

;; ATTORNEY/AGENT INFORMATION:

;; NAME: No. 5698403land, Greta E.

;; REGISTRATION NUMBER: 35,302

;; REFERENCE/DOCKET NUMBER: 32781

;; TELEPHONE: (312) 474-6300

;; TELEFAX: (312) 474-0448

;; TELEX: 25-3658

;; INFORMATION FOR SEQ ID NO: 8:

;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 441 amino acids

;; TYPE: amino acid

;; TOPOLOGY: linear

;; MOLECULE TYPE: protein

;; US-08-483-140-8

Query Match 99.8%; Score 2354; DB 1; Length 441;

Best Local Similarity 99.8%; Pred. No. 9.8e-246;

Matches 440; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MVPKHLVFLCGLAVVPFDQYINPVAHMKSSAWVNIQVLMMAASFGQTKIPRGN 60

Db 1 MVPKHLVFLCGLAVVPFDQYINPVAHMKSSAWVNIQVLMMAASFGQTKIPRGN 60

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Db 61 GPYSVGCTDLMDFTNKGTFRLYYPSQDNDRLDTLWIPNKEYFWGLSKFLGTHWLMGNI 120

Qy 121 LRLFGSMTTPANNWSPLRPGKYPVVFVSHGLGAFRTLYSAIGIDLASHGFIVAAVEHR 180

Db 121 LRLFGSMTTPANNWSPLRPGKYPVVFVSHGLGAFRTLYSAIGIDLASHGFIVAAVEHR 180

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Db 181 DRSATYYPKQSAAEIGDKSWLYLRTLKQEEETHIRNEQVORAKESQALSILID 240

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Db 421 NINTTNOHIMLQNSSGIEKYN 441

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RESULT 5
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; Sequence 8, Application US/08485938A
; Patent No. 5847088
; GENERAL INFORMATION:
; APPLICANT: Cousens, Lawrence S.
; APPLICANT: Eberhardt, Christine D.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Le Trong, Hai
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor
; TITLE OF INVENTION: Acetylhydrolase
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,938A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/318,905
; FILING DATE: 06-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 06-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5847088and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/32792
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3658
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 441 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-485-938A-8

Query Match 99.8%; Score 2354; DB 2; Length 441;
Best Local Similarity 99.8%; Pred. No. 9.8e-246;
Matches 440; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MWPVKLVLCGCLAVVYFDFQWQYINPVVHMKSSAWVVKIQVLMMAASFGQTKIPRGN 60
DB 1 MWPVKLVLCGCLAVVYFDFQWQYINPVVHMKSSAWVVKIQVLMMAASFGQTKIPRGN 60
QY 61 GPYSVGCTDLMPHTNKGTFRLRYLPPSQDNDRLDTLWIPNKEYFWGLSKFLGTHWLMGNI 120
DB 61 GPYSVGCTDLMPHTNKGTFRLRYLPPSQDNDRLDTLWIPNKEYFWGLSKFLGTHWLMGNI 120
QY 121 LRLFGSMTPANWNSPLRGEKYPVVFVSHGLGAFETLYSAIGIDIASHGFTVAVEHR 180
DB 121 LRLFGSMTPANWNSPLRGEKYPVVFVSHGLGAFETLYSAIGIDIASHGFTVAVEHR 180
QY 181 DRASATYYPKDSAAEIGDKSWLYLRTLKQEBETHIRNEQVQRAKECSQALSLLIDID 240
DB 181 DRASATYYPKDSAAEIGDKSWLYLRTLKQEBETHIRNEQVQRAKECSQALSLLIDID 240

RESULT 6
US-08-910-041-8
; Sequence 8, Application US/08910041
; Patent No. 5977308
; GENERAL INFORMATION:
; APPLICANT: Cousens, Lawrence S.
; APPLICANT: Eberhardt, Christine D.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Le Trong, Hai
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor
; TITLE OF INVENTION: Acetylhydrolase
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/910,041
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/483,232
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/318,905
; FILING DATE: 06-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 06-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Rin-Laures, Li-Hsien
; REGISTRATION NUMBER: 33,547
; REFERENCE/DOCKET NUMBER: 27866/34026
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3658
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 441 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-910-041-8

241 HGKPVKNALDLKFDMEQLKDSIDREKIAVIGHSGGATVIQTLSEQRFRCGIALDAWMF 300
241 HGKPVKNALDLKFDMEQLKDSIDREKIAVIGHSGGATVIQTLSEQRFRCGIALDAWMF 300
QY 301 PLGDEVYSRIPOPLFFINSEYFOYPANIIKMKCYSPDKERKMITIRGSHQNFADFTFA 360
DB 301 PLGDEVYSRIPOPLFFINSEYFOYPANIIKMKCYSPDKERKMITIRGSHQNFADFTFA 360
QY 361 TGIIGHMLKLGKGDIDSNKASLAFLOKHLGLHDKDFQWDCLEGGDDENLIPGT 420
DB 361 TGIIGHMLKLGKGDIDSNKASLAFLOKHLGLHDKDFQWDCLEGGDDENLIPGT 420
QY 421 NINTNQHIMLQNSGIEKYN 441
DB 421 NINTNQHIMLQNSGIEKYN 441
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Query Match 99.8%; Score 2354; DB 2; Length 441;
 Best Local Similarity 99.8%; Pred. No. 9.8e-246;
 Matches 440; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 M V P P K L H V L F C L C G C L A V Y P F D M Q Y I N P V A H M K S S A W N K I Q V L M A A S F G Q T K I P R G N 60
 D b 1 M V P P K L H V L F C L C G C L A V Y P F D M Q Y I N P V A H M K S S A W N K I Q V L M A A S F G Q T K I P R G N 60

Qy 61 G P Y S V G C T D L M F D H T N K G T F L R L Y Y P S Q D N D R L D T L M I P N K E Y F W G L S K F L G T H W L M G N I 120
 D b 61 G P Y S V G C T D L M F D H T N K G T F L R L Y Y P S Q D N D R L D T L M I P N K E Y F W G L S K F L G T H W L M G N I 120

Qy 121 L R L L F G S M T T P A N W N S P L R P G E K Y P L V V F S H G L G A F R T L Y S A I G I D L A S H G F I V A A V E H R 180
 D b 121 L R L L F G S M T T P A N W N S P L R P G E K Y P L V V F S H G L G A F R T L Y S A I G I D L A S H G F I V A A V E H R 180

Qy 181 D R S A S A T Y Y F K D Q S A A E I G D K S W L Y L R T L K Q E E T H I R N E O V R A K E C S Q A L S I L D I D 240
 D b 181 D R S A S A T Y Y F K D Q S A A E I G D K S W L Y L R T L K Q E E T H I R N E O V R A K E C S Q A L S I L D I D 240

Qy 241 H G K P V K N A L D L K F D M E Q L K D S I D R E K I A V I G H S F G G A T V I O T L S E D Q R F R C G I A L D A W M F 300
 D b 241 H G K P V K N A L D L K F D M E Q L K D S I D R E K I A V I G H S F G G A T V I O T L S E D Q R F R C G I A L D A W M F 300

Qy 301 P L G D E V Y S R I P Q P L F F I N S E Y F Q P A N I I K M K C Y S P D K E R K M I T I R G S V H Q N F A D F T F A 360
 D b 301 P L G D E V Y S R I P Q P L F F I N S E Y F Q P A N I I K M K C Y S P D K E R K M I T I R G S V H Q N F A D F T F A 360

Qy 361 T G K I I G H M L K L G D I D S N A A I D L S N K A S L A F L Q K H L G L H K D F D W D C L I E G D D E N L I P G T 420
 D b 361 T G K I I G H M L K L G D I D S N A A I D L S N K A S L A F L Q K H L G L H K D F D W D C L I E G D D E N L I P G T 420

Qy 421 N I N T T N Q H I M L Q N S S G I E K Y N 441
 D b 421 N I N T T N Q H I M L Q N S S G I E K Y N 441

RESULT 7

US-09-328-474-8
 ; Sequence 8, Application US/09328474
 ; Patent No. 6045794
 ; GENERAL INFORMATION:
 ; APPLICANT: Cousens, Lawrence S.
 ; APPLICANT: Eberhardt, Christine D.
 ; APPLICANT: Gray, Patrick W.
 ; APPLICANT: Le Trong, Hai
 ; APPLICANT: Tjoelker, Larry W.
 ; APPLICANT: Wilder, Cheryl L.
 ; TITLE OF INVENTION: Platelet-Activating Factor
 ; TITLE OF INVENTION: Acetylhydrolase
 ; NUMBER OF SEQUENCES: 30
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 ; STREET: 6300 Sears Tower, 233 South Wacker Drive
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: United States of America
 ; ZIP: 60606-6402
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/328,474
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/483,232
 ; FILING DATE: 07-JUN-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/318,905
 ; FILING DATE: 06-OCT-1994

PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/133,803
 ; FILING DATE: 06-OCT-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Rin-Laures, Li-Hsien
 ; REGISTRATION NUMBER: 33,547
 ; REFERENCE/DOCKET NUMBER: 27866/34026
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (312) 474-6300
 ; TELEFAX: (312) 474-0448
 ; TELEX: 25-3658
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 441 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-09-328-474-8

Query Match 99.8%; Score 2354; DB 3; Length 441;
 Best Local Similarity 99.8%; Pred. No. 9.8e-246;
 Matches 440; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 M V P P K L H V L F C L C G C L A V Y P F D M Q Y I N P V A H M K S S A W N K I Q V L M A A S F G Q T K I P R G N 60
 D b 1 M V P P K L H V L F C L C G C L A V Y P F D M Q Y I N P V A H M K S S A W N K I Q V L M A A S F G Q T K I P R G N 60

Qy 61 G P Y S V G C T D L M F D H T N K G T F L R L Y Y P S Q D N D R L D T L M I P N K E Y F W G L S K F L G T H W L M G N I 120
 D b 61 G P Y S V G C T D L M F D H T N K G T F L R L Y Y P S Q D N D R L D T L M I P N K E Y F W G L S K F L G T H W L M G N I 120

Qy 121 L R L L F G S M T T P A N W N S P L R P G E K Y P L V V F S H G L G A F R T L Y S A I G I D L A S H G F I V A A V E H R 180
 D b 121 L R L L F G S M T T P A N W N S P L R P G E K Y P L V V F S H G L G A F R T L Y S A I G I D L A S H G F I V A A V E H R 180

Qy 181 D R S A S A T Y Y F K D Q S A A E I G D K S W L Y L R T L K Q E E T H I R N E O V R A K E C S Q A L S I L D I D 240
 D b 181 D R S A S A T Y Y F K D Q S A A E I G D K S W L Y L R T L K Q E E T H I R N E O V R A K E C S Q A L S I L D I D 240

Qy 241 H G K P V K N A L D L K F D M E Q L K D S I D R E K I A V I G H S F G G A T V I O T L S E D Q R F R C G I A L D A W M F 300
 D b 241 H G K P V K N A L D L K F D M E Q L K D S I D R E K I A V I G H S F G G A T V I O T L S E D Q R F R C G I A L D A W M F 300

Qy 301 P L G D E V Y S R I P Q P L F F I N S E Y F Q P A N I I K M K C Y S P D K E R K M I T I R G S V H Q N F A D F T F A 360
 D b 301 P L G D E V Y S R I P Q P L F F I N S E Y F Q P A N I I K M K C Y S P D K E R K M I T I R G S V H Q N F A D F T F A 360

Qy 361 T G K I I G H M L K L G D I D S N A A I D L S N K A S L A F L Q K H L G L H K D F D W D C L I E G D D E N L I P G T 420
 D b 361 T G K I I G H M L K L G D I D S N A A I D L S N K A S L A F L Q K H L G L H K D F D W D C L I E G D D E N L I P G T 420

Qy 421 N I N T T N Q H I M L Q N S S G I E K Y N 441
 D b 421 N I N T T N Q H I M L Q N S S G I E K Y N 441

RESULT 8
 US-09-100-546-8
 ; Sequence 8, Application US/09100546
 ; Patent No. 6099836
 ; GENERAL INFORMATION:
 ; APPLICANT: Cousens, Lawrence S.
 ; APPLICANT: Eberhardt, Christine D.
 ; APPLICANT: Gray, Patrick W.
 ; APPLICANT: Le Trong, Hai
 ; APPLICANT: Tjoelker, Larry W.
 ; APPLICANT: Wilder, Cheryl L.
 ; TITLE OF INVENTION: Platelet-Activating Factor
 ; TITLE OF INVENTION: Acetylhydrolase
 ; NUMBER OF SEQUENCES: 30
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 ; STREET: 6300 Sears Tower, 233 South Wacker Drive

CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/100,546
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/010,715
FILING DATE:
FILING DATE: 06-OCT-1994
APPLICATION NUMBER: US 08/318,905
FILING DATE: 06-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,803
FILING DATE: 06-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: No. 6099836and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/32793
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3658
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 441 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-100-546-8

Query Match 99.8%; Score 2354; DB 3; Length 441;
Best Local Similarity 99.8%; Pred. No. 9.8e-246;
Matches 440; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	MVPPKLVLCGCLAVVYFDQYINPVAHMKSSAWVNKIQVLMMAASFGQTKIPRGN	60
Db	1	MVPPKLVLCGCLAVVYFDQYINPVAHMKSSAWVNKIQVLMMAASFGQTKIPRGN	60
QY	61	GPYSVGCTDLMFHTNKGTFRLRYPSQDNDRDLTLWIPNKEYFWGLSKFLGTHWLMGNI	120
Db	61	GPYSVGCTDLMFHTNKGTFRLRYPSQDNDRDLTLWIPNKEYFWGLSKFLGTHWLMGNI	120
QY	121	LRLFGSMTPPANWNSPLRPGKYPVVFVSHGLGAFRTLYSAIGIDLASHGFIVAAVEHR	180
Db	121	LRLFGSMTPPANWNSPLRPGKYPVVFVSHGLGAFRTLYSAIGIDLASHGFIVAAVEHR	180
QY	181	DRSASATYFKDQSAAEIGDKSWLYLRTLKQEBETHIRNEQVRQRAKCSQALSILID	240
Db	181	DRSASATYFKDQSAAEIGDKSWLYLRTLKQEBETHIRNEQVRQRAKCSQALSILID	240
QY	241	HGKPVKNALDKFDMQLKDSIDREKIAVIGHSGFGATVITLSEDRFCGIALDAWMF	300
Db	241	HGKPVKNALDKFDMQLKDSIDREKIAVIGHSGFGATVITLSEDRFCGIALDAWMF	300
QY	301	PLGDEVYSRIPOPLFFINSEYFOYPANIIMKKCYSPDKERKMITIRGSHQNFADPTFA	360
Db	301	PLGDEVYSRIPOPLFFINSEYFOYPANIIMKKCYSPDKERKMITIRGSHQNFADPTFA	360
QY	361	TGKIIGHMLKLKGDIDNSNAIDLSNKASLAFLOKHGLHDKDFQWDCCLIEGDDENLIPGT	420
Db	361	TGKIIGHMLKLKGDIDNSNAIDLSNKASLAFLOKHGLHDKDFQWDCCLIEGDDENLIPGT	420
QY	421	NINTTNOHIMLQNSSGIEKYN 441	
Db	421	NINTTNOHIMLQNSSGIEKYN 441	

RESULT 9
US-09-010-715-8
Sequence 8, Application US/09010715
Patent No. 6146625
GENERAL INFORMATION:
APPLICANT: Cousens, Lawrence S.
APPLICANT: Eberhardt, Christine D.
APPLICANT: Gray, Patrick W.
APPLICANT: Le Trong, Hai
APPLICANT: Tjoelker, Larry W.
APPLICANT: Wilder, Cheryl L.
TITLE OF INVENTION: Platelet-Activating Factor
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,715
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/318,905
FILING DATE: 06-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/133,803
FILING DATE: 06-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: No. 6146625and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/32793
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3658
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 441 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-010-715-8

Query Match 99.8%; Score 2354; DB 3; Length 441;
Best Local Similarity 99.8%; Pred. No. 9.8e-246;
Matches 440; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	MVPPKLVLCGCLAVVYFDQYINPVAHMKSSAWVNKIQVLMMAASFGQTKIPRGN	60
Db	1	MVPPKLVLCGCLAVVYFDQYINPVAHMKSSAWVNKIQVLMMAASFGQTKIPRGN	60
QY	61	GPYSVGCTDLMFHTNKGTFRLRYPSQDNDRDLTLWIPNKEYFWGLSKFLGTHWLMGNI	120
Db	61	GPYSVGCTDLMFHTNKGTFRLRYPSQDNDRDLTLWIPNKEYFWGLSKFLGTHWLMGNI	120
QY	121	LRLFGSMTPPANWNSPLRPGKYPVVFVSHGLGAFRTLYSAIGIDLASHGFIVAAVEHR	180
Db	121	LRLFGSMTPPANWNSPLRPGKYPVVFVSHGLGAFRTLYSAIGIDLASHGFIVAAVEHR	180
QY	181	DRSASATYFKDQSAAEIGDKSWLYLRTLKQEBETHIRNEQVRQRAKCSQALSILID	240
Db	181	DRSASATYFKDQSAAEIGDKSWLYLRTLKQEBETHIRNEQVRQRAKCSQALSILID	240

Qy 241 HGKPVKNALDLKFDMEQLKDSIDREKIAVIGHSGGATVIOTLSEDFRCGIALDAWMP 300
 Db 241 HGKPVKNALDLKFDMEQLKDSIDREKIAVIGHSGGATVIOTLSEDFRCGIALDAWMP 300
 Qy 301 PLGDEVYSRIPOPLFFINSEYFQYPANIIKMKKCYSPDKERKMITIRGSHVQNFADTFPA 360
 Db 301 PLGDEVYSRIPOPLFFINSEYFQYPANIIKMKKCYSPDKERKMITIRGSHVQNFADTFPA 360
 Qy 361 TGIIGHMLKLGKIDSNAAIDLSNKASLAFLOKHGLHKKDFDQWDCLEGGDENLIPGT 420
 Db 361 TGIIGHMLKLGKIDSNVAIDLSNKASLAFLOKHGLHKKDFDQWDCLEGGDENLIPGT 420
 Qy 421 NINTNQHIMLQNSGGIEKYN 441
 Db 421 NINTNQHIMLQNSGGIEKYN 441
 RESULT 10
 US-09-577-758-8
 ; Sequence 8, Application US/09577758
 ; Patent No. 6203790
 ; GENERAL INFORMATION:
 ; APPLICANT: Cousens, Lawrence S.
 ; APPLICANT: Eberhardt, Christine D.
 ; APPLICANT: Gray, Patrick W.
 ; APPLICANT: Le Trong, Hai
 ; APPLICANT: Tjoelker, Larry W.
 ; APPLICANT: Wilder, Cheryl L.
 ; TITLE OF INVENTION: Platelet-Activating Factor
 ; TITLE OF INVENTION: Acetylhydrolase
 ; NUMBER OF SEQUENCES: 30
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 ; STREET: 6300 Sears Tower, 233 South Wacker Drive
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: United States of America
 ; ZIP: 60606-6402
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/577,758
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 09/010,715
 ; FILING DATE:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/133,803
 ; FILING DATE: 06-OCT-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: No. 6203790and, Greta E.
 ; REGISTRATION NUMBER: 35,302
 ; REFERENCE/DOCKET NUMBER: 27866/32793
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (312) 474-6300
 ; TELEFAX: (312) 474-0448
 ; TELEX: 25-3658
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 441 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-09-577-758-8
 ; Query Match 99.8%; Score 2354; DB 3; Length 441;
 ; Best Local Similarity 99.8%; Pred. No. 9,8e-246;
 ; Matches 440; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MVRPKLHVLCCLGCLAVVYPPDMQYINPVAHMKSSAWNVKIQVLMMAASFGQTKIPRGN 60
 Db 1 MVRPKLHVLCCLGCLAVVYPPDMQYINPVAHMKSSAWNVKIQVLMMAASFGQTKIPRGN 60
 Qy 61 GPYSVGCTDLMFDFHTNKGTFRLYYPSQDNDRDLDTLMPNKEYFWGLSKFLGTHWLMGNI 120
 Db 61 GPYSVGCTDLMFDFHTNKGTFRLYYPSQDNDRDLDTLMPNKEYFWGLSKFLGTHWLMGNI 120
 Qy 121 LRLFGSMTPPANWNSPLRPGKEYPLVVFVSHGLGAFRTLYSAIGIDILASHGFIIVAAVHR 180
 Db 121 LRLFGSMTPPANWNSPLRPGKEYPLVVFVSHGLGAFRTLYSAIGIDILASHGFIIVAAVHR 180
 Qy 181 DRASATYYFKDQSAAEIGDKSMWLYLRTLKQEBETHIRNEQVORORAKESQALSILIDID 240
 Db 181 DRASATYYFKDQSAAEIGDKSMWLYLRTLKQEBETHIRNEQVORORAKESQALSILIDID 240
 Qy 241 HGKEVKNALDLKFDMEQLKDSIDREKIAVIGHSGGATVIOTLSEDFRCGIALDAWMP 300
 Db 241 HGKEVKNALDLKFDMEQLKDSIDREKIAVIGHSGGATVIOTLSEDFRCGIALDAWMP 300
 Qy 301 PLGDEVYSRIPOPLFFINSEYFQYPANIIKMKKCYSPDKERKMITIRGSHVQNFADTFPA 360
 Db 301 PLGDEVYSRIPOPLFFINSEYFQYPANIIKMKKCYSPDKERKMITIRGSHVQNFADTFPA 360
 Qy 361 TGIIGHMLKLGKIDSNAAIDLSNKASLAFLOKHGLHKKDFDQWDCLEGGDENLIPGT 420
 Db 361 TGIIGHMLKLGKIDSNVAIDLSNKASLAFLOKHGLHKKDFDQWDCLEGGDENLIPGT 420
 Qy 421 NINTNQHIMLQNSGGIEKYN 441
 Db 421 NINTNQHIMLQNSGGIEKYN 441
 RESULT 11
 US-08-485-938A-33
 ; Sequence 33, Application US/08485938A
 ; Patent No. 5847088
 ; GENERAL INFORMATION:
 ; APPLICANT: Cousens, Lawrence S.
 ; APPLICANT: Eberhardt, Christine D.
 ; APPLICANT: Gray, Patrick W.
 ; APPLICANT: Le Trong, Hai
 ; APPLICANT: Tjoelker, Larry W.
 ; APPLICANT: Wilder, Cheryl L.
 ; TITLE OF INVENTION: Platelet-Activating Factor
 ; TITLE OF INVENTION: Acetylhydrolase
 ; NUMBER OF SEQUENCES: 36
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 ; STREET: 6300 Sears Tower, 233 South Wacker Drive
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: United States of America
 ; ZIP: 60606-6402
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/485,938A
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 435
 ; FILING DATE: 06-OCT-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: No. 5847088and, Greta E.
 ; REGISTRATION NUMBER: 35,302
 ; REFERENCE/DOCKET NUMBER: 27866/32792

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (312) 474-6300
 TELEFAX: (312) 474-0448
 TELEX: 25-3658
 FILING DATE: 6-OCT-1994
 PRIOR APPLICATION DATA: US 08/133,803
 FILING DATE: 6-OCT-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: No. 5698403and, Greta E.
 REGISTRATION NUMBER: 35,302
 REFERENCE/DOCKET NUMBER: 32781
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (312) 474-6300
 TELEFAX: (312) 474-0448
 TELEX: 25-3658
 INFORMATION FOR SEQ ID NO: 28:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 444 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-485-938A-33

Query Match 83.3%; Score 1964.5; DB 2; Length 444;
 Best Local Similarity 82.4%; Pred. No. 1.4e-203;
 Matches 364; Conservative 39; Mismatches 38; Indels 1; Gaps 1;

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QY 1 MYPKHLVLCGLCLAVVPPDQVYNPVAHMKSSAWNKIQVLMMAASFGQTKIPRGN 60
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QY 61 GYSVSGCTDLMFDTNKGTFRLRYPSQDNDRLDITLWIPNKEYFWGLSKFLGTHWLMGNI 120
DB 61 GYSVSGCTDLMFDTNKGTFRLRYPSQDNDRLDITLWIPNKEYFWGLSKFLGTHWLMGKI 120
QY 121 LRLFGSMTTPANNWSPRLPGEKYPLVVFHSHGLGAFRTLYSAIGIDLASHGFIVAAVEHR 180
DB 121 MGLFFSGMTTPAANWHLRTGEKYPLIFSHGLGAFRTLYSAIGIDLASHGFIVAAVEHR 180
QY 181 DRSASATYFKQDSAAEIGDKSWLYLRTLQO-BEETHIRNEQVORAKESQALSILDI 239
DB 181 DGSASATYFKQDSAAEIGDKSWLYLRTLQO-BEETHIRNEQVORAKESQALSILDI 240
QY 240 DHGKPVNMDLKPDMEQKDSIDREKIAVIGHSGFAGTIVQTLSEDFRCGIALDAMW 299
DB 241 DHGKPVNMDLKPDMEQKDSIDREKIAVIGHSGFAGTIVQTLSEDFRCGIALDAMW 300
QY 300 FPLGDEVYSRIPQPLFFINSEYFOYPANIIKMKKCYSPDKERKMITIRGSHVQNFADFTF 359
DB 301 FPLGDEVYSRIPQPLFFINSEYFOYPANIIKMKKCYSPDKERKMITIRGSHVQNFADFTF 360
QY 360 ATGKIIGHMLKLGDIIDNSNAIDLSNKASLAFLOKHLGLHKDPDQWDLLEGDDENLIPG 419
DB 361 ATGKIIGHMLKLGDIIDNSNAIDLSNKASLAFLOKHLGLHKDPDQWDLLEGDDENLIPG 420
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DB 421 TNINTNQHIMLQNSSGIERPN 442

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RESULT 12
 US-08-483-140-28
 Sequence 28, Application US/08483140
 Patent No. 5698403
 GENERAL INFORMATION:
 APPLICANT: ICOS Corporation
 TITLE OF INVENTION: Platelet-Activating Factor Acetyl
 TITLE OF INVENTION: Hydrolase
 NUMBER OF SEQUENCES: 30
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Marshall, O'Toole, Gertein, Murray & Borun
 STREET: 6300 Sears Tower, 233 South Wacker Drive
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60606
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/483,140
 FILING DATE:

CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/318,905
 FILING DATE: 6-OCT-1994
 PRIOR APPLICATION DATA: US 08/133,803
 FILING DATE: 6-OCT-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: No. 5698403and, Greta E.
 REGISTRATION NUMBER: 35,302
 REFERENCE/DOCKET NUMBER: 32781
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (312) 474-6300
 TELEFAX: (312) 474-0448
 TELEX: 25-3658
 INFORMATION FOR SEQ ID NO: 28:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 444 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-483-140-28

Query Match 82.1%; Score 1935.5; DB 1; Length 444;
 Best Local Similarity 80.8%; Pred. No. 2e-200;
 Matches 357; Conservative 38; Mismatches 46; Indels 1; Gaps 1;

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DB 61 GYSVSGCTDLMFDTNKGTFRLRYPSQDNDRLDITLWIPNKEYFWGLSKFLGTHWLMGKI 120
QY 121 LRLFGSMTTPANNWSPRLPGEKYPLVVFHSHGLGAFRTLYSAIGIDLASHGFIVAAVEHR 180
DB 121 LRFPSGVTTPANNWSPRLPGEKYPLVVFHSHGLGAFRTLYSAIGIDLASHGFIVAAVEHR 180
QY 181 DRSASATYFKQDSAAEIGDKSWLYLRTLQO-BEETHIRNEQVORAKESQALSILDI 239
DB 181 DGSASATYFKQDSAAEIGDKSWLYLRTLQO-BEETHIRNEQVORAKESQALSILDI 240
QY 240 DHGKPVNMDLKPDMEQKDSIDREKIAVIGHSGFAGTIVQTLSEDFRCGIALDAMW 299
DB 241 DHGKPVNMDLKPDMEQKDSIDREKIAVIGHSGFAGTIVQTLSEDFRCGIALDAMW 300
QY 300 FPLGDEVYSRIPQPLFFINSEYFOYPANIIKMKKCYSPDKERKMITIRGSHVQNFADFTF 359
DB 301 LPLDDAIYSRIPQPLFFINSEYFOYPANIIKMKKCYSPDKERKMITIRGSHVQNFADFTF 360
QY 360 ATGKIIGHMLKLGDIIDNSNAIDLSNKASLAFLOKHLGLHKDPDQWDLLEGDDENLIPG 419
DB 361 TTGKIIVGYITFLKGDIDNSNAIDLSNKASLAFLOKHLGLHKDPDQWDLLEGDDENLIPG 420
QY 420 TNINTNQHIMLQNSSGIEKYN 441
DB 421 TNINTNQHIMLQNSSGIERPN 442

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RESULT 13
 US-08-485-938A-32
 Sequence 32, Application US/08485938A
 Patent No. 5847088
 GENERAL INFORMATION:
 APPLICANT: Cousins, Lawrence S.
 APPLICANT: Eberhardt, Christine D.
 APPLICANT: Gray, Patrick W.
 APPLICANT: Le Trong, Hai
 APPLICANT: Tjoelker, Larry W.
 APPLICANT: Wilder, Cheryl L.
 TITLE OF INVENTION: Platelet-Activating Factor
 TITLE OF INVENTION: Acetylhydrolase

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 15, 2005, 10:07:52 ; Search time 131.868 Seconds
(without alignments)
1103.088 Million cell updates/sec

Title: US-09-922-067F-14
Perfect score: 2358
Sequence: 1 MPPKLVFLCGLAVVY.....INTNQHIMLQNSGIEKYN 441

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1396920 seqs, 329844858 residues

Total number of hits satisfying chosen parameters: 1396920

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubaa/US06_PUBCOMB.pep.*
- 4: /cgn2_6/ptodata/1/pubaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubaa/US08_PUBCOMB.pep.*
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- 10: /cgn2_6/ptodata/1/pubaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubaa/US11_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/1/pubaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2358	100.0	441	16	US-10-741-601-373
2	2358	100.0	441	16	US-10-741-601-374
3	2354	99.8	441	9	US-09-729-402-8
4	2354	99.8	441	14	US-10-003-978A-8
5	2354	99.8	441	14	US-10-161-127-1
6	2354	99.8	441	16	US-10-755-889-278
7	797	33.8	392	10	US-09-961-253-3
8	747	31.7	392	10	US-09-961-253-1
9	497	21.1	384	15	US-10-369-493-5034
10	493.5	20.9	476	15	US-10-369-493-6760
11	295.5	12.5	438	15	US-10-369-493-2350
12	205	8.7	439	15	US-10-354-437-112
13	202	8.6	401	14	US-10-156-761-8015

14	186	7.9	37	9	US-09-922-067-1	Sequence 1, Appli
15	186	7.9	37	14	US-10-173-233-1	Sequence 1, Appli
16	186	7.9	37	14	US-10-406-156-1	Sequence 1, Appli
17	170	7.2	30	9	US-09-922-067-2	Sequence 2, Appli
18	170	7.2	30	14	US-10-173-233-2	Sequence 2, Appli
19	170	7.2	30	14	US-10-406-156-2	Sequence 2, Appli
20	163	6.9	407	14	US-10-156-761-8357	Sequence 8357, Ap
21	122.5	5.2	273	15	US-10-369-493-11644	Sequence 11644, A
22	122.5	5.2	273	15	US-10-369-493-15162	Sequence 15162, A
23	122.5	5.2	273	15	US-10-369-493-15162	Sequence 15162, A
24	115	4.9	352	14	US-10-102-239-5	Sequence 5, Appli
25	114.5	4.9	262	14	US-10-102-239-7	Sequence 7, Appli
26	114.5	4.9	315	15	US-10-424-599-188557	Sequence 188557,
27	111	4.7	301	14	US-10-102-239-4	Sequence 4, Appli
28	110.5	4.7	262	14	US-10-102-239-6	Sequence 6, Appli
29	110.5	4.7	739	15	US-10-282-122A-53623	Sequence 53623, A
30	108	4.6	622	9	US-09-966-803-2	Sequence 2, Appli
31	106.5	4.5	275	15	US-10-289-762-181	Sequence 181, App
32	104.5	4.4	868	15	US-10-282-122A-77289	Sequence 77289, A
33	104	4.4	20	9	US-09-922-067-11	Sequence 11, Appl
34	104	4.4	20	14	US-10-173-233-11	Sequence 11, Appl
35	104	4.4	20	14	US-10-406-156-11	Sequence 11, Appl
36	104	4.4	27	9	US-09-922-067-3	Sequence 3, Appli
37	104	4.4	27	14	US-10-173-233-3	Sequence 3, Appli
38	104	4.4	27	14	US-10-406-156-3	Sequence 3, Appli
39	103.5	4.4	473	15	US-10-369-493-13571	Sequence 13571, A
40	103.5	4.4	931	15	US-10-369-493-22397	Sequence 22397, A
41	103.5	4.4	931	16	US-10-723-807-11	Sequence 11, Appl
42	103.5	4.4	1153	16	US-10-437-963-140880	Sequence 140880,
43	103	4.4	790	15	US-10-369-493-3803	Sequence 3803, Ap
44	102	4.3	330	15	US-10-425-114-36813	Sequence 36813, A
45	102	4.3	684	15	US-10-425-114-57854	Sequence 57854, A

ALIGNMENTS

RESULT 1
US-10-741-601-373
; Sequence 373, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: STENOSIS, METHODS OF DETECTION AND USES THEREOF
; CURRENT APPLICATION NUMBER: US/10/741,601
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 26415
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 373
; LENGTH: 441
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-741-601-373

Query Match	100.0%;	Score	2358;	DB	16;	Length	441;
Best Local Similarity	100.0%;	Pred. NO.	1.5e-226;				
Matches	441;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						
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Db	1	MVPPKLVFLCGLAVVYFDFWQYINPVAHKKSSAWNKIQVLMMAASFGQTKIPRGN	60				
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Db	61	GPSVSGCTDLMFHDTNKGTFRLRYPSQDNDRLDTLWIPNKEYFWGLSKFGLTHTWLMGNI	120				
Qy	121	LRLFLGSMTPANWNSPLRPGCKYPLVVFHSHGLGAFRTLYSAIGIDLASHGFIVAAVEHR	180				
Db	121	LRLFLGSMTPANWNSPLRPGCKYPLVVFHSHGLGAFRTLYSAIGIDLASHGFIVAAVEHR	180				
Qy	181	DRSASATYFKDQSAASIGDKSWLYLRTLKQEBETHRNEQVROBAKESQALSILIDID	240				

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Db 181 DRASATYFKDQSAABIGDKSWLYLRLTKQEBETHIRNEQVRQRAKESQALSILID 240
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Db 241 HGKPVKNALDKFDMEQLKDSIDREKIAVIGHSGFGGATVIQTLSEDFRCGIALDAWMF 300
Qy 301 PLGDEVYSRIPOPLFFINSEYFQYPANIIRKMKCYSPDKERKMITIRGSHQNFADPTFA 360
Db 301 PLGDEVYSRIPOPLFFINSEYFQYPANIIRKMKCYSPDKERKMITIRGSHQNFADPTFA 360
Qy 361 TGLIIGHMLKLGDISNAIDLSNKASLAFLOKHLGLHKDFQWDCCLIEGDDENLIPGT 420
Db 361 TGLIIGHMLKLGDISNAIDLSNKASLAFLOKHLGLHKDFQWDCCLIEGDDENLIPGT 420
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Db 421 NINTTNOHIMLQNSGGIEKYN 441

RESULT 2
US-10-741-601-374
; Sequence 374, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: STENOSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CU001500
; CURRENT APPLICATION NUMBER: US/10/741,601
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 26415
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 374
; LENGTH: 441
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-741-601-374

Query Match 100.0%; Score 2358; DB 16; Length 441;
Best Local Similarity 100.0%; Pred. No. 1.5e-226;
Matches 441; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MVPPKLVLCGCLAVVYPPDWQYINPVAHMKSSAWVNKIQVLMMAASFGQTKIPRGN 60
Qy 61 GPYSVGCTDLMFDTNKGTFRLRYPSQDNDRLDTLWIPNKEYFWGLSKFLGTHWLMGNI 120
Db 61 GPYSVGCTDLMFDTNKGTFRLRYPSQDNDRLDTLWIPNKEYFWGLSKFLGTHWLMGNI 120
Qy 121 LRLFGSMTPPANWNSPLRPGKYPVLFVSHGLGAFRTLYSAIGIDLASHGFIVAAVEHR 180
Db 121 LRLFGSMTPPANWNSPLRPGKYPVLFVSHGLGAFRTLYSAIGIDLASHGFIVAAVEHR 180
Qy 181 DRASATYFKDQSAABIGDKSWLYLRLTKQEBETHIRNEQVRQRAKESQALSILID 240
Db 181 DRASATYFKDQSAABIGDKSWLYLRLTKQEBETHIRNEQVRQRAKESQALSILID 240
Qy 241 HGKPVKNALDKFDMEQLKDSIDREKIAVIGHSGFGGATVIQTLSEDFRCGIALDAWMF 300
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Qy 361 TGLIIGHMLKLGDISNAIDLSNKASLAFLOKHLGLHKDFQWDCCLIEGDDENLIPGT 420
Db 361 TGLIIGHMLKLGDISNAIDLSNKASLAFLOKHLGLHKDFQWDCCLIEGDDENLIPGT 420
Qy 421 NINTTNOHIMLQNSGGIEKYN 441
Db 421 NINTTNOHIMLQNSGGIEKYN 441

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Db 421 NINTTNOHIMLQNSGGIEKYN 441

RESULT 3
US-09-729-402-8
; Sequence 8, Application US/09729402
; Patent No. US20010021379A1
; GENERAL INFORMATION:
; APPLICANT: Cousens, Lawrence S.
; Eberhardt, Christine D.
; Gray, Patrick W.
; Le Trong, Hai
; Tjoelker, Larry W.
; Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor
; Acetylhydrolase
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/729,402
; FILING DATE: 04-Dec-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/318,905
; FILING DATE: 06-OCT-1994
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 06-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. US20010021379A1and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/32793
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3658
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 441 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-729-402-8

Query Match 99.8%; Score 2354; DB 9; Length 441;
Best Local Similarity 99.8%; Pred. No. 3.9e-226;
Matches 440; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 1 MVPPKLVLCGCLAVVYPPDWQYINPVAHMKSSAWVNKIQVLMMAASFGQTKIPRGN 60
Qy 61 GPYSVGCTDLMFDTNKGTFRLRYPSQDNDRLDTLWIPNKEYFWGLSKFLGTHWLMGNI 120
Db 61 GPYSVGCTDLMFDTNKGTFRLRYPSQDNDRLDTLWIPNKEYFWGLSKFLGTHWLMGNI 120
Qy 121 LRLFGSMTPPANWNSPLRPGKYPVLFVSHGLGAFRTLYSAIGIDLASHGFIVAAVEHR 180
Db 121 LRLFGSMTPPANWNSPLRPGKYPVLFVSHGLGAFRTLYSAIGIDLASHGFIVAAVEHR 180
Qy 181 DRASATYFKDQSAABIGDKSWLYLRLTKQEBETHIRNEQVRQRAKESQALSILID 240
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Db 301 PLGDEVYSRIPOPLFFINSEYFOYPANIIMKKKCYSPDKERKMITIRGSHVQNFADFTFA 360

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Db 361 TGKIIIGHMLKLGKIDNSNAIDLSNKASLAFLOKHLGLHKDFQWDCLIEGDDENLIPGT 420

Qy 421 NINTTNOHIMLQNSSGIEKYN 441

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RESULT 6

US-10-755-889-278

Sequence 278, Application US/10755889

Publication No. US20040171823A1

GENERAL INFORMATION:

APPLICANT: Bristol-Myers Squibb Company

TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-KB

FILE REFERENCE: D0284 NP

CURRENT APPLICATION NUMBER: US/10755,889

CURRENT FILING DATE: 2004-01-13

PRIOR APPLICATION NUMBER: U.S. 60/440,068

PRIOR FILING DATE: 2003-01-14

PRIOR APPLICATION NUMBER: U.S. 60/469,757

PRIOR FILING DATE: 2003-05-12

NUMBER OF SEQ ID NOS: 823

SOFTWARE: Patent in version 3.2

SEQ ID NO 278

LENGTH: 441

TYPE: PRT

ORGANISM: Homo sapiens

US-10-755-889-278

Query Match 99.8%; Score 2354; DB 16; Length 441;

Best Local Similarity 99.8%; Pred. No. 3.9e-226;

Mismatches 0; Conservative 0; Indels 0; Gaps 0;

Qy 1 MVEPKHLVLCGCLAVVYFPDQYINPVAHMKSSAWNKIQVLMAAASFGQTKIPRGN 60

Db 1 MVEPKHLVLCGCLAVVYFPDQYINPVAHMKSSAWNKIQVLMAAASFGQTKIPRGN 60

Qy 61 GPVSVGCTDLMFDHNTKGTFLRLYYPSQDNDRLDTLWIPNKEYFWGLSKFLGTHWLMGNI 120

Db 61 GPVSVGCTDLMFDHNTKGTFLRLYYPSQDNDRLDTLWIPNKEYFWGLSKFLGTHWLMGNI 120

Qy 121 LRLFGSMTTPANNWNSPLRPGCKYPLVVFVSHGLGAFRTLYSAIGIDLASHGFIIVAAVEHR 180

Db 121 LRLFGSMTTPANNWNSPLRPGCKYPLVVFVSHGLGAFRTLYSAIGIDLASHGFIIVAAVEHR 180

Qy 181 DRASATYFKDQSAABIGDKSWLYLRLTKQEBETHIRNEQVRORAKECSQALSILIID 240

Db 181 DRASATYFKDQSAABIGDKSWLYLRLTKQEBETHIRNEQVRORAKECSQALSILIID 240

Qy 241 HGKPVKNALDKFDMEOQKSIDREKIAVIGHSGFGGATVIQTLSQDORFRGIALDAWMF 300

Db 241 HGKPVKNALDKFDMEOQKSIDREKIAVIGHSGFGGATVIQTLSQDORFRGIALDAWMF 300

Qy 301 PLGDEVYSRIPOPLFFINSEYFOYPANIIMKKKCYSPDKERKMITIRGSHVQNFADFTFA 360

Db 301 PLGDEVYSRIPOPLFFINSEYFOYPANIIMKKKCYSPDKERKMITIRGSHVQNFADFTFA 360

Qy 361 TGKIIIGHMLKLGKIDNSNAIDLSNKASLAFLOKHLGLHKDFQWDCLIEGDDENLIPGT 420

Db 361 TGKIIIGHMLKLGKIDNSNAIDLSNKASLAFLOKHLGLHKDFQWDCLIEGDDENLIPGT 420

Qy 421 NINTTNOHIMLQNSSGIEKYN 441

Db 421 NINTTNOHIMLQNSSGIEKYN 441

RESULT 7

US-09-961-253-3

Sequence 3, Application US/09961253

Publication No. US20030040093A1

GENERAL INFORMATION:

APPLICANT: ADACHI, HIDEKI

TSUJIMOTO, MASAFUMI

ARAI, HIROYUKI

INOUE, KEIZO

TITLE OF INVENTION: PLATELET ACTIVATING FACTOR

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,

P.C.

STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400

CITY: ARLINGTON

STATE: VA

COUNTRY: USA

ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/961,253

FILING DATE: 25-Sep-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/196,222

FILING DATE: <Unknown>

APPLICATION NUMBER: US 08/886,152

FILING DATE: 30-JUN-1997

APPLICATION NUMBER: JP 8-188369

FILING DATE: 28-JUN-1996

ATTORNEY/AGENT INFORMATION:

NAME: OBLON, NORMAN F.

REGISTRATION NUMBER: 24,618

REFERENCE/DOCKET NUMBER: 2292-041-0

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-413-3000

TELEFAX: 703-413-2220

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 392 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

ORIGINAL SOURCE:

ORGANISM: HUMAN

SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-09-961-253-3

Query Match 33.8%; Score 797; DB 10; Length 392;

Best Local Similarity 43.5%; Pred. No. 1.6e-70;

Mismatches 163; Conservative 71; Indels 12; Gaps 6;

Qy 57 PRGNPYSVCGTDLMDHTNKGTFRLRYPSQDNDRL--DTLWIPNKEYFWGLSKFLGTH 114
Db 10 PVTGPHLVGCDVMEQNLGSGFRFLFYPCQKAEETWEQPLWIPRYEICTGLAEYLOFN 69
Qy 115 WLMGNIL-RLLFSGMTTPANWNSPLRPGKEK-YPLVWFVSHGLGAFRTLYSAIGIDLASHGF 172
Db 70 KRCGGLLFNLAAGSCRLPVSWMNGPFTKDSGYPLIIFSHGLGAFRTLYSAFCMELASRGF 129
Qy 173 IVAAVEHRDRSASATYYFK-----DQSAAEIGDKSWLYLRLTKQ-BEETHIRNEQVRORA 226
Db 130 VVAVPEHRDRSAAATYFCKQAPENQPTNESLOEWEIPFRVEREKEKEFHVNRNPQVHORV 189
Qy 227 KECQALSLILDIDHGRPKVNALDKFDMEOQKDSIDREKIAVIGHSGFGGATVIOTLSED 286
Db 190 SECVRLKILQEVTAGQVFNILPGGLDMLTKGNIDMSRVAVVMGHSFGGATAILALAKE 249
Qy 287 QRFRGIALDAMFPLGDEVYSRIPQPLFFINSYFQYPANIIKMKKCYSPDKERKMITI 346
Db 250 TQFRCAVALDAMFPLERDPYPKARGPVFFINTEKFTQTMESVNLKMKKICAQHEQSRITV 309
Qy 347 RGSVHONFADPTFATGKIIGHML--KLKGDIDSNAADLSNKASIAFLQKHLGHLKDFDQ 404
Db 310 LGSVHRSQTDPAFVTGNLIGKFFSTETGRSLDPYEGQEVVMVRAMLAFQKHLDLKEDYQ 369
Qy 405 WDCLEGGDENLIPG 419
Db 370 WNNLIEGIGPSLTPG 384

RESULT 8

US-09-961-253-1

; Sequence 1, Application US/09961253

; Publication No. US20030040093A1

; GENERAL INFORMATION:

; APPLICANT: TSUCHI, HIDEKI

; ARAI, HIROYUKI

; INOUE, KEIZO

; TITLE OF INVENTION: PLATELET ACTIVATING FACTOR

; ACETYLHYDROLASE, AND GENE THEREOF

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: OBLON, SPIVAK, MCCELLAND, MAIER & NEUSTADT,

; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400

; CITY: ARLINGTON

; STATE: VA

; COUNTRY: USA

; ZIP: 22202

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/961,253

; FILING DATE: 25-Sep-2001

; CLASSIFICATION: <Unknown>

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: US/09/196,222

; FILING DATE: <Unknown>

; APPLICATION NUMBER: US 08/896,152

; FILING DATE: 30-JUN-1997

; APPLICATION NUMBER: JP 8-188369

; FILING DATE: 28-JUN-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: OBLON, NORMAN F.

; REGISTRATION NUMBER: 24,618

; REFERENCE/DOCKET NUMBER: 2292-041-0

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 703-413-3000

; TELEFAX: 703-413-2220

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 392 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: BOVINE (Bos taurus)
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-961-253-1

Query Match 31.7%; Score 747; DB 10; Length 392;
Best Local Similarity 41.9%; Pred. No. 1.6e-65;
Matches 157; Conservative 67; Mismatches 139; Indels 12; Gaps 6;
Qy 57 PRGNPYSVCGTDLMDHTNKGTFRLRYPSQDNDRL--DTLWIPNKEYFWGLSKFLGTH 114
Db 10 PVTGPHLVGCDVMEQNLGSGFRFLFYPCQKAEETWEQPLWIPRYEICTGLAEYLOFN 69
Qy 115 WLMGNIL-RLLFSGMTTPANWNSPLRPGKEK-YPLVWFVSHGLGAFRTLYSAIGIDLASHGF 172
Db 70 KRCGGLLFNLAAGSCRLPVSWMNGPFTKDSGYPLIIFSHGMGAFRTVYSAFCMELASRGF 129
Qy 173 IVAAVEHRDRSASATYYFK-----DQSAAEIGDKSWLYLRLTKQ-BEETHIRNEQVRORA 226
Db 130 VVAVPEHRDRSAAATCFCKQTPENQPDNEAKENIPHQIEGEKEFEYVRYNQVHORV 189
Qy 227 KECQALSLILDIDHGRPKVNALDKFDMEOQKDSIDREKIAVIGHSGFGGATVIOTLSED 286
Db 190 SECVRLKILQEVTAGQVFNILPGGLDMLTKGGIDVSRVAVVMGHSFGGATAILALAKE 249
Qy 287 QRFRGIALDAMFPLGDEVYSRIPQPLFFINSYFQYPANIIKMKKCYSPDKERKMITI 346
Db 250 MQRCAVALDAMFPLEHDFYPTARGPIFFINASKFQTVETVNLMMKKICDQHOSRIITV 309
Qy 347 RGSVHONFADPTFATGKIIGHMLK--LKGDIDSNAADLSNKASIAFLQKHLGHLKDFDQ 404
Db 310 LGSVHRSQTDPAFVAGNWSKFFSSHTRGSLDPYEGQETVVRAMLAFQKHLDLKEDYQ 369
Qy 405 WDCLEGGDENLIPG 419
Db 370 WNNLIEGIGPSLTPG 384

RESULT 9

US-10-369-493-5034

; Sequence 5034, Application US/10369493

; Publication No. US20030233675A1

; GENERAL INFORMATION:

; APPLICANT: Cao, Yongwei

; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Slater, Steven C.

; APPLICANT: Goldman, Barry S.

; APPLICANT: Chen, Xianfeng

; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

; FILE REFERENCE: 38-10(52052)B

; CURRENT APPLICATION NUMBER: US/10/369,493

; CURRENT FILING DATE: 2003-02-28

; PRIOR APPLICATION NUMBER: US 60/360,039

; PRIOR FILING DATE: 2002-02-21

; NUMBER OF SEQ ID NOS: 47374

; SEQ ID NO 5034

; LENGTH: 384

; TYPE: PRT

; ORGANISM: Caenorhabditis elegans

US-10-369-493-5034

Query Match 21.1%; Score 497; DB 15; Length 384;
Best Local Similarity 33.9%; Pred. No. 1.6e-40;
Matches 118; Conservative 74; Mismatches 140; Indels 16; Gaps 9;
Qy 55 KIPRNGPYSVCGTDLMDPDH-TNKGTFRLRYPSQDNDRLD----TLWIPNKEYFWGLSK 109

Db 14 KMP---GQFVGCMDLMEBAAGSLFMRFFPT-DSEITGPSSLPVWIPRPEYAVGGE 69
QY 110 FLG-TWLMGNILRLFLGSMTPPANWNSPL-RPEKYPLVVFSHGLGAFRTLYSAIGIDL 167
Db 70 YLGHSPHQMDLISLVLGDKKVCIDNAQSTKDKWPLVFSHGLGSGRTFYSTYCTSL 129
QY 168 ASHGFIVAAEHRDRSASATYFYKDSAAHIGDKSWLYLRTLKQEBETHIRNEQVORAK 227
Db 130 ASHGYYVAAEHRDSSACWYKLVKNGTLVEKPMKIKLVDRNDKQDFKIRNEQVGRAE 189
QY 228 ECSQALSILIDHKGKVPKALDI--KFDMEQLKDSIDREKIAVIGHSGFAGATVIQTLSE 285
Db 190 ECAKAVKILQOLSGN-VKDKVIIGNANLEFFKKNKLLTTTASIIHSGFGATSIASSSS 248
QY 286 DQPRCGIADAWMFFLGDDEVYRIPQPLFINSEYFOYFYPANIIKMKKCYSPDKERKMIT 345
Db 249 D--FQKALVDGWNYPDLQNOQEQAKQPIFNLVGDWQWNNENLEVMRKILPNEGNILLT 306
QY 346 IRGSHQNFADFTFATGKIIGHMLKLKGDIDSNAAIDLSNKAFLAQ 393
Db 307 LSGAVHQSFTDFPFVFNWLAQFGVHGTPPEYLCMQSAIETLSFLK 354
RESULT 10
US-10-369-493-6760
; Sequence 6760, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US/10/369,493
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 6760
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-10-369-493-6760

Query Match 20.98; Score 493.5; DB 15; Length 476;
Best Local Similarity 32.18; Pred. No. 4.9e-40;
Matches 123; Conservative 69; Mismatches 154; Indels 37; Gaps 8;
QY 37 AWNKIQVMAAASFGQTKIPRGNGPYSGVCTDLMPDHT--NKGTFRLRYPSQNDRL 93
Db 75 SYSSPQVLTRQVS-----GQFVGCKLMDIGTVLGRGLFMRLYFT-DSQAA 123
QY 94 D----TLWIPNKEYFWGLSKPLG-TWLMGNILRLFLGSMTPPANWNSPLRPG-EKYPLV 147
Db 124 DISSYPLWLPKPYAHGLGEVLGQSSQKMNVTITVVGREKDCIENAOQSTKCKWPIV 183
QY 148 VFSHGLGAFRTLYSAIGIDLSHGHFIVAAEH-----RDRSASATYFK 191
Db 184 VFSHGLGSGRTFYSTYCTSLASHGYYVAAEVHKWKGSGGRCRDHVFSCRDHSACWTYQLT 243
QY 192 DQAAAEIGDKSWLYLRTLKQEBETHIRNEQVORAKESQALSILIDHKG-PVKNALD 250
Db 244 EKNGLVEQPIKIKLEKNEKNEFKRNQVGRVTECVKALNVQLNLGTVPEKVLIG 303
QY 251 LKFDMEQLKDSIDREKIAVIGHSGFAGATVIQTLSEDOQRFRCGIALDAMFPLGDEVYSRI 310
Db 304 NDYNWAQFKNLVMSASVIGHSGFGATSLASSAYTTDFQKALVFDGWMYPLDSTQOEQA 363
QY 311 PQPLFFINSEYFOYFYPANIIKMKKCYSPDKERKMITIRGSHQNFADFTFATGKIIGHMLK 370

Db 364 KQPTFLNVGDWQWNNENLDVMKKIISHNDGNLALTNGAVHQCFSDPFPIFSPWLAKKFG 423
QY 371 LKGDIDSNAAIDLSNKAFLAQ 393
Db 424 VQGRTPSLCMQAAIBLSLAFLE 446
RESULT 11
US-10-369-493-2350
; Sequence 2350, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 2350
; LENGTH: 438
; TYPE: PRT
; ORGANISM: Schizosaccharomyces pombe
US-10-369-493-2350

Query Match 12.5%; Score 295.5; DB 15; Length 438;
Best Local Similarity 24.8%; Pred. No. 2.7e-20;
Matches 112; Conservative 84; Mismatches 141; Indels 115; Gaps 22;
QY 55 KIPRGNGPYSGV-----CTDLMFDTNKGTFRLRYV---PSQD-NDRLDTLW 97
Db 10 QLPAYCGPLPVGSLVLELSVPEFRCEYKTIETKHLRTVKVRIEYPLDPTKDVPEPTDELW 69
QY 98 IPNKEYFWGLSKPLGTHLMGNILRLFLGSMTPPANWNSPLRPG-----KYPLVVF 149
Db 70 LPFHEGIDEVAK--GFRW---LIRAPASGLT---NLALFVYKGEFLHPPNNGKLPVFIF 121
QY 150 SHGLGAFRTLYSAIGIDLSHGHFIVAAEHRDRSA-----SATYFKDQSAE 197
Db 122 SHGLVGRNVYSSLCGTIASYGVIVLAMEHRDNSAIISTRDPLHPPEEPYVQYR---E 178
QY 198 IGDKSWLYLRTLKQEBETHIRNEQVORAKESQALSILIDI-DHGPVKVX-----ALDL 251
Db 179 ISD-----FYADATVVLQNERLLFRQOEIQIALQMIIRNINDLGTDPENLPLCSVDS 230
QY 252 KF---DMEQLKDSID--REKIAVIGHSGFAGATV-----IOTLSED---QRFRCGIAL 295
Db 231 SFYNSVFGSKMGNLTAQGLIVAGHSFGAATCAFTSGSKSLYNDYMEHTEFKSILY 290
QY 296 DAMMFLGDEVYSRIPQP-LFFINSEYFOYFYPANIIKMKCY-----SPDKERK 342
Db 291 DIWMLPVRQLHLSTMYPTLMIISYEFRRFVDNFQALSWLVNKSQENQVAGSADKMS 350
QY 343 MITIR-----GSVHQNFADFTFATGKIIGHMLKLKGDIDSNAAIDLSNKAFLAQ 393
Db 351 VVPLKKYSHVYVDGTVHANQSDPLILLPRMVLRLKGRFEADPYEALINTRSSVQFLR 410
QY 394 KHLGLHKDPQWDCLLTEGDE-----NLIPG 419
Db 411 EN---HVE-----NVQGNDFSSLQTNIPG 433
RESULT 12
US-10-354-437-112
; Sequence 112, Application US/10354437
; Publication No. US20040023257A1

RESULT 13
US-10-156-761-8015
; Sequence 8015, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEGA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/922,067
FILING DATE: 03-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/193,130
FILING DATE: 1998-11-17
APPLICATION NUMBER: PCT/GB94/01374
FILING DATE: 24 June 1994
ATTORNEY/AGENT INFORMATION:
NAME: Dustman, Wayne J.
REGISTRATION NUMBER: 33,870
REFERENCE/DOCKET NUMBER: P30693
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5023
TELEFAX: 610-270-5090
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
FEATURE:
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-922-067-1

Query Match 7.9%; Score 186; DB 9; Length 37;
Best Local Similarity 100.0%; Pred. No. 5.2e-11;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 368 MLKLKGDIDSNAAIDLSNKASLAPLQKHLGLHKDFDQ 404
Db 1 MLKLKGDIDSNAAIDLSNKASLAPLQKHLGLHKDFDQ 37

RESULT 15

US-10-173-233-1
Sequence 1, Application US/10173233
Publication No. US20030148398A1
GENERAL INFORMATION:
APPLICANT: MacPhee, Colin Houston
Tew, David Graham
Southan, Christopher Donald
Hickey, Dierdre Mary Bernadette
Gloger, Israel Simon
Lawrence, Geoffrey Mark Prouse
Rice, Simon Quentyn John
TITLE OF INVENTION: Compounds
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/173,233
FILING DATE: 14-Jun-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/569,899
FILING DATE: 12-May-2000
ATTORNEY/AGENT INFORMATION:
NAME: Dustman, Wayne J.
REGISTRATION NUMBER: 33,870
REFERENCE/DOCKET NUMBER: P30693
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5023
TELEFAX: 610-270-5090
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
FEATURE:
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-173-233-1

Query Match 7.9%; Score 186; DB 14; Length 37;
Best Local Similarity 100.0%; Pred. No. 5.2e-11;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 368 MLKLKGDIDSNAAIDLSNKASLAPLQKHLGLHKDFDQ 404
Db 1 MLKLKGDIDSNAAIDLSNKASLAPLQKHLGLHKDFDQ 37

Search completed: March 15, 2005, 10:25:09
Job time : 132.868 secs

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OM protein - protein search, using sw model

Run on: March 15, 2005, 09:56:51 ; Search time 36.75 Seconds
(without alignments)
1154.601 Million cell updates/sec

Title: US-09-922-067f-14
Perfect score: 2358
Sequence: 1 MPPKLVHFLCGLAVV.....INTTNQHIMLQNSSGIEKYN 441

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2354	99.8	441	2 S60247	platelet-activatin
2	1572.5	66.7	436	2 JC5021	platelet-activatin
3	497	21.1	384	2 T32756	hypothetical prote
4	493.5	20.9	476	2 T28936	hypothetical prote
5	295.5	12.5	438	2 T39268	hypothetical prote
6	249.5	10.6	450	2 G83740	hypothetical prote
7	162.5	6.9	546	2 D83408	hypothetical prote
8	153.5	6.5	348	2 A82876	conserved hypothet
9	149	6.3	391	2 T36311	probable lipase
10	148.5	6.3	795	2 F82858	dipeptidyl-peptida
11	125.5	5.3	395	2 A82606	conserved hypothet
12	125.5	5.3	395	2 F97388	probable lipase (A
13	125	5.3	545	2 A82062	hypothetical prote
14	122.5	5.2	275	2 B98301	non-heme chloroper
15	122.5	5.2	275	2 A82982	non-heme chloroper
16	120.5	5.1	310	2 JN0490	28K lipase precurs
17	120	5.1	543	2 AF1927	hypothetical prote
18	117.5	5.0	622	2 S75452	hypothetical prote
19	116.5	4.9	314	2 AF3193	conserved hypothet
20	112	4.7	286	2 D75217	probable 2-acetyl-
21	110.5	4.7	711	2 S66261	X-Pro dipeptidyl-p
22	110	4.7	622	2 F71174	hypothetical prote
23	108.5	4.6	326	2 T36421	hypothetical prote
24	107	4.5	367	2 S19172	cytochrome P450 2B
25	106.5	4.5	275	2 A86511	acyltransferase fa
26	106.5	4.5	275	2 G72111	dienelactone hydro
27	106	4.5	632	2 E75057	peptidase PAB1418
28	104.5	4.4	868	2 G82193	aminopeptidase N V
29	103.5	4.4	931	2 A49737	dipeptidyl aminope

RESULT 1

S60247

Platelet-activating factor acetylhydrolase precursor - human

C:Species: Homo sapiens (man)

C:Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004

C:Accession: S60247

R:Tjoelker, L.W.; Wilder, C.; Eberhardt, C.; Stafforini, D.M.; Dietsch, G.; Schimpf, B.;

W. Nature 374, 549-553, (1995)

A:Title: Anti-inflammatory properties of a platelet-activating factor acetylhydrolase.

A:Reference number: S60247; MUID:95214779; PMID:7700381

A:Accession: S60247

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-441 <TJ0>

A:Cross-references: UNIPROT:Q13093; EMBL:U020157; NID:g780132; PIDN:AAC50126.1; PID:g7801

Query Match 99.8%; Score 2354; DB 2; Length 441;
Best Local Similarity 99.8%; Pred. No. 5.1e-178;
Matches 440; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	MVPPKLVHFLCGLAVVYFDFQYINPVAHMKSSAWNKIQVLMMAASFGQTKIPRGN	60
Db	1	MVPPKLVHFLCGLAVVYFDFQYINPVAHMKSSAWNKIQVLMMAASFGQTKIPRGN	60
Qy	61	GPYSVGCTDLMFDTNKGTFRLLYPSQDNDRLDTLIPNKEYFWGLSKFLGTHWLMGNI	120
Db	61	GPYSVGCTDLMFDTNKGTFRLLYPSQDNDRLDTLIPNKEYFWGLSKFLGTHWLMGNI	120
Qy	121	LRLFLGSMTPANWNSPLRPGCKYPLVVFVSHGLGAFRTLYSAIGIDLASHGFIVAAVEHR	180
Db	121	LRLFLGSMTPANWNSPLRPGCKYPLVVFVSHGLGAFRTLYSAIGIDLASHGFIVAAVEHR	180
Qy	181	DRSASATYFKDQSAABIGDKSWLYLRTLKQEBETHIRNEQVQRRAKESQALSILIDID	240
Db	181	DRSASATYFKDQSAABIGDKSWLYLRTLKQEBETHIRNEQVQRRAKESQALSILIDID	240
Qy	241	HGKPVKNALDLKFDMEQLKDSIDREKIAVIGHSGFGGATVIOTLSEDFRCGIALDAMWF	300
Db	241	HGKPVKNALDLKFDMEQLKDSIDREKIAVIGHSGFGGATVIOTLSEDFRCGIALDAMWF	300
Qy	301	PLGDEVYSRIPOPLFFINSEYFQYIPANIIMKKKCYSPDKERKMITIRGSVHONFADFTFA	360
Db	301	PLGDEVYSRIPOPLFFINSEYFQYIPANIIMKKKCYSPDKERKMITIRGSVHONFADFTFA	360
Qy	361	TGKIIGHMLKLKGDIDNSNAADLSNKSALFLOKHLGLHKDFDQWDCCLIEGDDENLIPGT	420
Db	361	TGKIIGHMLKLKGDIDNSNAADLSNKSALFLOKHLGLHKDFDQWDCCLIEGDDENLIPGT	420
Qy	421	NINTTNQHIMLQNSSGIEKYN	441
Db	421	NINTTNQHIMLQNSSGIEKYN	441

hypothetical prote
hypothetical prote
probable non-heme
probable ATP/GTP-b
hypothetical prote
hypothetical prote
cystathionine beta
hypothetical prote
choline-binding pr
dipeptidyl aminope
conserved hypothet
ATP-dependent clp
cystathionine beta
hypothetical prote
hypothetical prote
hypothetical prote
hypothetical prote

RESULT 2
JC5021
platelet-activating factor-acetylhydrolase (EC 3.1.1.-.-) precursor - guinea pig
N/Alternate names: PAR-acetylhydrolase
C/Species: Cavia porcellus (guinea pig)
C/Date: 30-Sep-1993 #sequence_revision 21-Jan-1997 #text_change 09-Jul-2004
C/Accession: JC5021; PC4207
R/Karasaawa, K.; Kuge, O.; Kawaasaki, K.; Nishijima, M.; Nakano, Y.; Tomita, M.; Yokoyama, J.; Biochem. 120, 838-844, 1996
A/Title: Cloning, expression and characterization of plasma platelet-activating factor-a
A/Reference number: JC5021; MUID:97103479; PMID:8947850
A/Accession: JC5021
A/Molecule type: DNA
A/Residues: 1-436 <KAR1>
A/Cross-references: UNIPROT:P70683; DDBJ:D67037; NID:g1644228; PIDN:BAAL1054.1; PID:g164
A/Accession: PC4207
A/Molecule type: protein
A/Residues: 123-129;134-139;208-217;258-264;332-337;341-345;346-361;373-384;385-392 <KAR
A/Experimental source: liver
C/Comment: This enzyme converts platelet-activating factor to an inactive metabolite lys
C/Keywords: glycoprotein, hydrolase
F/1-21/Domain: signal sequence #status predicted <SIG>
F/22-436/Product: platelet-activating factor-acetylhydrolase #status predicted <MAT>
F/76,200,324/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 66.7%; Score 1572.5; DB 2; Length 436;
Best Local Similarity 66.2%; Pred. No. 2:5e-116; Indels 7; Gaps 2;
Matches 292; Conservative 63; Mismatches 79; Indels 7; Gaps 2;

QY 1 MVPPKLVLCGLAVVYFDFQYINPVVAHMKSSAWNVKIQVMAAASFGQTKIPRGN 60
DB 1 MAPPKLHTLCLSGFALVHPFDWRDLDPVYIQSSWVQRIQSELLITFSGHTTIPKGN 60
QY 61 GPYSVGCTDLMFHTNKGTLRLYPSQDNDRLDTLWPNKEYFWGLSKFLGTHLMGNI 120
DB 61 GPYSVGCTDLMGTYNQSSFLRLYPSQDNDFFDALWPNKEYFQGLTGLASSFLGKL 120
QY 121 LRLFLGSMTPANWNSPLRPGKVPVPLVPSHGLGAPRTLYSAIGIDLASHGFVAVEHR 180
DB 121 LKLLYGVKVPKWNPLKTEKGLPLIFSHGLGAFRSYSAIGIELASHGFVAVEHR 180
QY 181 DRASATYYPKDOAAEIGDKSWLYLTLKQEBETHIRNEQVRQRAKESQALSILIDID 240
DB 181 DESAAATYYPQDAPAAESGNKSMYIKV--GNLETEERKQLRQRGECQALSLLSID 238
QY 241 HGRPKVALDLKPDMEQLKDSIDREKIAVIGHSGFGGATVITLSEDOQRFRCGIALDAWMP 300
DB 239 EGEFPKVALDLNFDIQLKGLSDRSKVAIIGHSGFGGATVITLSEDOQRFRCGIALDPWMP 298
QY 301 PLGDEVYSRIPQPLFFINSYFQVPANIIKMKCYSPDKERKMITYRSHQNFADPTFA 360
DB 299 PVGEDVHAKIPQPLFFINSYFQSANDTKIEFYQPKERKMIAVKGSHVHNFVPTFA 358
QY 361 TGKIIHMLKGLGIDSNAAIDLNSKASLAFLOKHLGLHDFQWDCQLIEDDENLPGT 420
DB 359 TGKIIQMLKGLKIDSEVAMDINKASLAFLOKHLGLDNFQWDCQLIEDDENLPIEF 418
QY 421 NINTNQHIMLQNSGIEKN 441
DB 419 TIPTT-----MQSSTGTQERN 434

RESULT 3
T32756
hypothetical protein W03G9.6 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C/Accession: T32756
R/Dante, M.; Keppler, D.
submitted to the EMBL Data Library, December 1997
A/Description: The sequence of C. elegans cosmid W03G9.

A/Reference number: Z21220
A/Accession: T32756
A/Status: preliminary; translated from GB/EMBL/DDBJ
A/Molecule type: DNA
A/Residues: 1-384 <DAN>
A/Cross-references: UNIPROT:O44753; EMBL:AF039716; PIDN:AAB96738.1; GSPDB:GN00019; CESP:
A/Experimental source: strain Bristol N2; clone W03G9
C/Genetics:
A/Gene: CESP:W03G9.6
A/Map position: 1
A/Introns: 47/3; 90/2; 142/2; 183/3; 333/3

Query Match 21.1%; Score 497; DB 2; Length 384;
Best Local Similarity 33.9%; Pred. No. 1:7e-31;
Matches 118; Conservative 74; Mismatches 140; Indels 16; Gaps 9;

QY 55 KIPRNGPVSVCCTDLMFDH-TNKGTLRLYPSQDNDRLD----TLWIPNKYFWGLSK 109
DB 14 KMP---GQPKVGCMGLMIEEAGSGFLMFLPFT-DSEITGPSLSPLVWIPRPRYAYGVGE 69
QY 110 FLG-THWLMGNILRLFGSMTPANWNSPL-RPGKVPVPLVPSHGLGAPRTLYSAIGIDL 167
DB 70 YLGHSPHMDLISLVIGDKRVDICINAQLSTKSKWPLVPSHGLGSGRTFTYCTSL 139
QY 168 ASHGPIVAAVEHRDRSASATYYPKDOAAEIGDKSWLYLTLKQEBETHIRNEQVRQRAK 227
DB 130 ASHGVAVAVEHRDSSACWTYKLVKNGTLVEKPMKIKLVDRNDKQFKIRNEQVGKRAE 189
QY 228 ECSQALSILIDHGXFPKVALDL--KFDMEQLKDSIDREKIAVIGHSGFGGATVITLSE 285
DB 190 ECAKAVKILFQDLSGN-VKDKVIIGNNANLEFFPKNLLTTASIIIGHSGFGGATSIASSSS 248
QY 286 DQRFRCGIALDAMFPLGDEVYSRIPQPLFFINSYFQVPANIIKMKCYSPDKERKMITY 345
DB 249 D--FQKAVLDGHWYFLDQNOEQAKQPINFLNVGQWQNNENLEVRKILPNNEGNILLT 306
QY 346 IRGSHVQNFADFTFATGKIIGHMLKGLGIDSNAAIDLNSKASLAFLO 393
DB 307 LSGAVHQSFTDFPFVFPNWLAKQFVGHGTPYPLCMQSAIELTSLFLK 354

RESULT 4
T28936
hypothetical protein C52B9.7 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 18-Feb-2000
C/Accession: T28936
R/Nelson, J.
submitted to the EMBL Data Library, July 1996
A/Description: The sequence of C. elegans cosmid C52B9.
A/Reference number: Z20545
A/Accession: T28936
A/Status: preliminary; translated from GB/EMBL/DDBJ
A/Molecule type: DNA
A/Residues: 1-476 <NEL>
A/Cross-references: EMBL:U64598; PIDN:AAC4973.1; GSPDB:GN00028; CESP:C52B9.7
A/Experimental source: strain Bristol N2; clone C52B9
C/Genetics:
A/Gene: CESP:C52B9.7
A/Map position: X
A/Introns: 23/3; 70/2; 121/3; 164/2; 273/3; 343/3; 425/3

Query Match 20.9%; Score 493.5; DB 2; Length 476;
Best Local Similarity 32.1%; Pred. No. 4:4e-31;
Matches 123; Conservative 69; Mismatches 154; Indels 37; Gaps 8;

QY 37 AWNKIQVLMMAAASFGQTKIPRNGPVSVCCTDLMFDHT---NKGTFRLYPSQDNDRL 93
DB 75 SVTSPQVLTQRVS-----GQFQVQCKDLMDGTGLDGLGFLMRLYFPT-DSQAA 123
QY 94 D----TLWIPNKYFWGLSKFLG-THWLMGNILRLFGSMTPANWNSPLRPG-EKYPLV 147
DB 124 DISSYPLMLPKFYAHGLGELYQSSQKQNVITSTVVGKREDCIENAQMTCKDKWPIV 193

Qy 148 VFSHGLGAPRTLYSAIGIDILASHGFIIVAAVEH-----RDRSASATYFFK 191
Db 184 VFSHGLGSRFTYSTCTSLASHGCVVAAVEHKKWKGSGRCDHVAFA8CRDHSACWTYQLT 243
Qy 192 DOSAAEIGDKSWLYRLTKQEEETHIRNEQVRORAKESQALSILIDIDHKG-PVKNALD 250
Db 244 EKNGLVQPIKIKLIEKNEKNEFKIRNQGVKRTVCVKNALNVLEQLNGTVPKVLIG 303
Qy 251 LKPDMEQLKDSIDREKIAVGHSGFGATVITQTLSEDQRFRCGIALDAMFPPLGDEVYSRI 310
Db 304 NDYNWAQFKNLVMSASVGHSGFGATSLASSAYTTDFOKAIVDFGCMVPLDSTQEQEA 363
Qy 311 POPLFFINSEYFQYPAIIKKKCYSPDKERKMTIRGSHVONPADTFTATGKIIGHMLK 370
Db 364 KQPTFLNVGDQWQNEKLVNKKIISHNDGNLALTTLNGAVHQCFSPFPFPPSLAKKFG 423
Qy 371 LKGDIDSNAAIDLSNKASLAFLO 393
Db 424 VQGRTEFSLCQAAIELSLAFLE 446
RESULT 5
T39268
hypothetical protein SPBC106.11c - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T39268
R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Davis, P.; Churcher, C.M.
submitted to the EMBL Data Library, August 1999
A;Reference number: 221840
A;Accession: T39268
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-438 <LYN>
A;Cross-references: UNIPROT:Q9URV1; EMBL:AL110295; PIDN:CAB53727.1; GSPDB:GN00067; SPDB:
A;Experimental source: strain 972h-, cosmid c106
C;Genetics:
A;Gene: SPDB:SPBC106.11c
A;Map position: 2

Query Match 12.5%; Score 295.5; DB 2; Length 438;
Best Local Similarity 24.8%; Pred. No. 1.7e-15;
Matches 112; Conservative 84; Mismatches 141; Indels 115; Gaps 22;
Qy 55 KIPRNGPYSVG-----CTDLMPDHTNKGTFRLYY---PSQD-NDRLDTLW 97
Db 10 QLPAYCGPLPGSLVLELSPVEEFCVETIEHKLRTVKVIFYPPLDPTKQVPEPTDELW 69
Qy 98 IPNKEYFWGLSKFLGTHWLMGNILRLFGSWTTTPANNNSPLRPOE-----KYPLVVP 149
Db 70 LPFHEGIPVAK--GFRW---LLRAFASGLT---NLALPVYKGELFHPNNGKLPVFI 121
Qy 150 SHHIGAFRTLYSAIGIDILASHGFIIVAAVEHDSRA-----SATYFFKQSAAE 197
Db 122 SHLUGSRNVYSSLCGTIASGIVLAMEHEDNSAIIISVDRDPLHPPEPPVQYR---E 178
Qy 198 IGDKSWLYRLTKQEEETHIRNEQVRORAKESQALSILDI-DHKGPKVN-----ALDL 251
Db 179 ISD-----FYADATVVLQNERLLFRQEIQIALQWIRNINDLGTDPENLPLCSVDS 230
Qy 252 KF---DMEQLKDSID--REKIAVGHSGFGATV-----IQTUSED-----QRFRCGIAL 295
Db 231 SFYNSVFSQMKGNLTAQGEILVAGHSFGAATCAFISGSSTKSLYNDYMFHTEPKCSILY 290
Qy 296 DAWMFLGDEVYSRIPOP-LFFINSEYFQYPAIIKKKCY-----SPDKERK 342
Db 291 DIWMLPVRQLHLSTMRYPTLMIISYEFRRVDFNFOALESWLNVKDSNQNGESADSKMS 350
Qy 343 MITIR-----GSHVQNFADTFTATGKIIGHMLKLKGDIDSNAAIDLSNKASLAFLO 393
Db 351 VVPLKKYSHVVPVYDGTVHANSQDLPIILLPRMVLVKGKFPADPYEARLINTRSSVQFLR 410

Qy 394 KHLGLHKDPQWDCLIEGDDE-----NLIPG 419
Db 411 EN---HVE-----NVQGDNDPSSLQTNIIIPG 433
RESULT 6
G83740
hypothetical protein BH0727 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: G83740
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira,
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: G83740
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-450 <STO>
A;Cross-references: UNIPROT:Q9KEX2; GB:AP001509; GB:BA000004; NID:gl0173176; PIDN:BA0044
A;Experimental source: strain C-125
C;Genetics:
A;Gene: BH0727

Query Match 10.6%; Score 249.5; DB 2; Length 450;
Best Local Similarity 22.0%; Pred. No. 7.6e-12;
Matches 87; Conservative 75; Mismatches 122; Indels 111; Gaps 16;
Qy 56 IPRNGPYSVGCTDLMP-----DHTNKGTFRLYYPSQ-DNDRDLDTLWIPNKEYF 104
Db 112 LPEPTGPEYIGVTNFHWDPDREVEGVNGRNLWYPAELTEGLKAPAFDPSYT 171
Qy 105 WGLSKFLGTHWLMGNILRLFGSWTTTPAN--WNSPLRP-GEKYPVIVFVSHGLGAFRTLYS 161
Db 172 ELVSKELPYTY---KALLYSVIQTETHSFANVPVADHGAIPYVLLISPGYNSNFWYT 226
Qy 162 AIGDILASHGFIIVAAVEHDSASATYFFKQSAEIGDKSWLYRLTKQEEETHIRNEQ 221
Db 227 SQAETLASHGYIVCSIEH-----TYI-----TGLPTL--FPDGRIVVEQ 263
Qy 222 VQRAKESQALSILIDIDHKGPKVNAL-----DLKFDMEQLK-----DSIDR 264
Db 264 I-----DLEGRDLDEITVWVDVQVLDQLQKNWSDPQNLNGLRLDM 308
Qy 265 EKIAVGHSGFGATVITQTLSEDQRFRCGIALDAMFPPLGDEVYSRIPOPLFFINS----- 319
Db 309 DRVCMGLHSGFGATTAQVWHQDPRIRAGVNMVGDGLF--GSLIERGLDYPFMYMSGVEVS 366
Qy 320 -----EYFOYPAIIKKKCYSPDKERK-----MITIRGSHVQNFADTFTAT 361
Db 367 MEGPDGKKVBEAELEPE---EFREFIADDKRKGKALKNGLYVVIENAEHESFSDWMLYS 423
Qy 362 GKIIGHMLKLKGDIDSNAAIDLSNKASLAFLOKHL 396
Db 424 PLLLDRLDLP-----LDQINKTLDDFFDEHL 449

RESULT 7
D83408
hypothetical protein PA1907 [imported] - Pseudomonas aeruginosa (strain PA01)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: D83408
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br,
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: D83408
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-546 <STO>

RESULT 13

Db 180 REEFWRQCMGGLKQGLDSIRAFSESD-----FHQDLKAFDKPTVLVHGGDDQ 227

Qy 416 LIP 418

Db 228 IVP 230
::|

Search completed: March 15, 2005, 10:08:36
Job time : 39.75 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 15, 2005, 09:48:35 ; Search time 164.294 Seconds
(without alignments)
1374.528 Million cell updates/sec

Title: US-09-922-067F-14
Perfect score: 2358
Sequence: 1 MPPKLVFLCLCGCLAVV.....INTNQHIMLQNSGIEKYN 441

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03:*

1: uniprot_sprot;*

2: uniprot_trembl;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2354	99.8	441	1	PAPA HUMAN
2	1964.5	83.3	444	1	PAPA BOVIN
3	1935.5	82.1	444	1	PAPA CANFA
4	1572.5	66.7	436	1	PAPA CAVEPO
5	1556.5	66.0	440	2	Q921t4 mus musculu
6	1555.5	66.0	440	2	Q8BKW3
7	1514.5	64.2	440	1	PAPA MOUSE
8	1226.5	52.0	346	2	Q9DB74
9	1131.5	48.0	422	1	PAPA CHICK
10	1093	46.4	404	2	Q6NYI7
11	819	34.7	390	1	PAF2 RAT
12	809	34.3	390	1	PAF2 MOUSE
13	797	33.8	392	1	PAF2 HUMAN
14	747	31.7	392	1	PAF2 BOVIN
15	696	29.5	362	2	Q6GPX8
16	508.5	21.6	388	1	PAPA CABEL
17	497	21.1	384	2	Q44753
18	374.5	15.9	103	2	O6UB75
19	308	13.1	609	2	Q7S2B3
20	296	12.6	920	2	Q7URC4
21	295.5	12.5	438	2	Q9URV1
22	249.5	10.6	450	2	Q9KEX2
23	220	9.3	468	2	Q6HML0
24	214	9.1	468	2	Q81UC8
25	213	9.0	468	2	Q81H53
26	206.5	8.8	386	2	Q9FX29
27	202	8.6	401	2	Q82QM6
28	199	8.4	468	2	Q73CM7
29	188.5	8.0	456	2	Q81E25
30	184	7.8	402	2	Q70KJ6
31	174	7.4	331	2	Q7NJZ2 gloeobacter

32	166.5	7.1	378	2	Q65IY4
33	163	6.9	407	2	Q82FQ3
34	162.5	6.9	546	2	Q912U7
35	159.5	6.8	795	2	Q87FB4
36	153.5	6.5	348	2	Q8UCP7
37	149	6.3	391	2	Q92360
38	148.5	6.3	795	2	Q9PHC9
39	146.5	6.2	559	2	Q8DI73
40	141.5	6.0	372	2	Q8XUH7
41	136.5	5.8	345	2	Q7UU10
42	133	5.6	878	2	Q75C14
43	132.5	5.6	386	2	Q728I3
44	132	5.6	789	2	Q93M73
45	132	5.6	801	2	Q8P3Q3

ALIGNMENTS

RESULT 1

ID	PAPA HUMAN	STANDARD;	PRT;	441 AA.
AC	Q13093; Q15692; Q8IVA2;			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	Platelet-activating factor acetylhydrolase precursor (EC 3.1.1.47)			
DE	(PAF acetylhydrolase) (PAF 2-acylhydrolase) (LDL-associated			
DE	phospholipase A2) (LDL-PLA(2)) (2-acetyl-1-alkylglycerophosphocholine			
DE	esterase) (1-alkyl-2-acetyl-glycerophosphocholine esterase).			
GN	Name=PLA2G7; Synonyms=PAPAH;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 42-57.			
RC	TISSUE=Myeloid;			
RX	MEDLINE=95214779; PubMed=7700381; DOI=10.1038/374549a0;			
RA	Tjcelker L.W., Wilder C., Eberhardt C., Stafforini D.M., Dietsch G.,			
RA	Schimpf B., Hooper S., le Trong H., Cousins L.S., Zimmerman G.A.,			
RA	Yamada Y., McIntyre T.M., Prescott S.M., Gray P.W.;			
RT	"Anti-inflammatory properties of a platelet-activating factor			
RL	acetylhydrolase.";			
RN	[2]			
RP	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.			
RC	TISSUE=Lymphoma;			
RX	MEDLINE=96197208; PubMed=8624782;			
RA	Tew D.G., Southan C., Rice S.Q.J., Lawrence M.P., Li H., Boyd H.F.,			
RA	Moore K., Gloger I.S., Macphree C.H.;			
RT	"Purification, properties, sequencing, and cloning of a lipoprotein-			
RT	associated, serine-dependent phospholipase involved in the oxidative			
RT	modification of low-density lipoproteins.";			
RL	Arterioscler. Thromb. Vasc. Biol. 16:591-599 (1996).			
RN	[3]			
RP	SEQUENCE FROM N.A., AND VARIANT ALA-379.			
RC	TISSUE=Blood;			
RX	MEDLINE=22338257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heisch F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			

Q65IY4	bacillus li
Q82PQ3	streptomyce
Q912J7	pseudomonas
Q87FB4	xylella fas
Q8UCP7	agrobacteri
Q92360	streptomyce
Q9PHC9	xylella fas
Q8DI73	synchococc
Q8XUH7	raistonia s
Q7UU10	rhodopirell
Q75C14	ashbya goss
Q728I3	desulfovibr
Q93M73	xanthomonas
Q8P3Q3	xanthomonas

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Maria M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RL and mouse cDNA sequences.",
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RP [4]
 RP MUTAGENESIS.
 RP MEDLINE=96029630; PubMed=7592717; DOI=10.1074/jbc.270.43.25481;
 RA Tjoelker L.W., Eberhardt C., Unger J., le Trong H., Zimmerman G.A.,
 RA McIntyre T.M., Stafforini D.M., Prescott S.M., Gray P.W.,
 RT "Plasma platelet-activating factor acetylhydrolase is a secreted
 RL phospholipase A2 with a catalytic triad.",
 RL J. Biol. Chem. 270:25481-25487 (1995).
 RN [5]
 RP VARIANT PLA2G7 DEFICIENCY PHR-279.
 RP MEDLINE=96259525; PubMed=8675689;
 RA Stafforini D.M., Satoh K., Akimatsu D.L., Tjoelker L.W., Eberhardt C.,
 RA Yoshida H., Imaizumi T., Takamatsu S., Zimmerman G.A., McIntyre T.M.,
 RA Gray P.W., Prescott S.M.,
 RT "Platelet-activating factor acetylhydrolase deficiency. A missense
 RT mutation near the active site of an anti-inflammatory phospholipase.",
 RL J. Clin. Invest. 97:2784-2791 (1996).
 RN [6]
 RP VARIANT PLA2G7 DEFICIENCY ARG-281.
 RP MEDLINE=97396177; PubMed=9245731; DOI=10.1006/bbr.1997.7047;
 RA Yamada Y., Yokota M.,
 RA "Loss of activity of plasma platelet-activating factor acetylhydrolase
 RT due to a novel Gln281-->Arg mutation.",
 RL Biochem. Biophys. Res. Commun. 236:772-775 (1997).
 RN [7]
 RP VARIANT PLA2G7 DEFICIENCY PHR-279.
 RP MEDLINE=98074100; PubMed=9412624;
 RA Hiramoto M., Yoshida H., Imaizumi T., Yoshimizu N., Satoh K.,
 RT "A mutation in plasma platelet-activating factor acetylhydrolase
 RT (Val279-->Phe) is a genetic risk factor for stroke.",
 RL Stroke 28:2417-2420 (1997).
 RN [8]
 RP VARIANT PLA2G7 DEFICIENCY PHR-279.
 RP MEDLINE=98132308; PubMed=9472966;
 RA Yamada Y., Ichihara S., Fujimura T., Yokota M.,
 RT "Identification of the G994-->T missense in exon 9 of the plasma
 RT platelet-activating factor acetylhydrolase gene as an independent risk
 RT factor for coronary artery disease in Japanese men.",
 RL Metabolism 47:177-181 (1998).
 RN [9]
 RP VARIANT PLA2G7 DEFICIENCY PHR-279.
 RP MEDLINE=98430412; PubMed=9759612;
 RA Yoshida H., Imaizumi T., Fujimoto K., Itaya H., Hiramoto M.,
 RA Yoshimizu N., Fukushi K., Satoh K.,
 RT "A mutation in plasma platelet-activating factor acetylhydrolase
 RT (Val279Phe) is a genetic risk factor for cerebral hemorrhage but not
 RT for hypertension.",
 RL Thromb. Haemost. 80:372-375 (1998).
 RN [10]
 RP VARIANTS HIS-92; THR-198 AND ALA-379.
 RP MEDLINE=20311534; PubMed=10733466;
 RA Kruse S., Mac X.-Q., Heinzmann A., Blattmann S., Robertes M.H.,
 RA Braun S., Gao P.-S., Forster J., Hopkin J.M., Shirakawa T.,
 RA Daichmann K.A.,
 RT "The Ile198Thr and Ala379Val variants of plasmatic PAF-acetylhydrolase
 RT impair catalytic activities and are associated with atopy and
 RT asthma.",
 RL Am. J. Hum. Genet. 66:1522-1530 (2000).
 CC -1- FUNCTION: Modulates the action of platelet-activating factor (PAF)
 CC by hydrolyzing the sn-2 ester bond to yield the biologically
 CC inactive lyso-PAF. Has a specificity for substrates with a short
 CC residue at the sn-2 position. It is inactive against long-chain
 CC phospholipids.
 CC -1- CATALYTIC ACTIVITY: 1-alkyl-2-acetyl-sn-glycero-3-phosphocholine +
 CC H(2)O = 1-alkyl-sn-glycero-3-phosphocholine + acetate.
 CC -1- SUBCELLULAR LOCATION: Extracellular.
 CC -1- TISSUE SPECIFICITY: Plasma.

CC -1- POLYMORPHISM: The alleles Thr-198 and Val-379 are associated with
 CC atopy and asthma.
 CC -1- DISEASE: Defects in PLA2G7 are the cause of platelet-activating
 CC factor acetylhydrolase deficiency (PLA2G7 deficiency)
 CC [MIM:601690]. It is a trait which is present in 27% of Japanese.
 CC It could have a significant physiologic effect in the presence of
 CC inflammatory bodily responses.
 CC -1- SIMILARITY: Belongs to the AB hydrolase superfamily. Lipase
 CC family.
 CC -----
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 CC -----
 CC EMBL; U20157; AAC50126.1; -;
 CC EMBL; U24577; AAB04170.1; -;
 CC EMBL; BC038452; AAH38452.1; -;
 CC PIR; S60247; S60247.
 CC Genew; HGNC:9040; PLA2G7.
 CC MIM; 601690; -;
 CC GO; GO:0005576; C:extracellular; TAS.
 CC GO; GO:0005543; F:phospholipid binding; TAS.
 CC GO; GO:0006954; P:inflammatory response; TAS.
 CC GO; GO:0006629; P:lipid metabolism; TAS.
 CC InterPro; IPR008262; Lipase_AS.
 CC InterPro; IPR005085; PAF_Ac_hydrol_II.
 CC InterPro; IPR000379; Ser_estrs.
 CC Pfam; PF03403; PAF-AH_P_II; 1.
 CC PROSITE; PS01120; LIPASE_SER; 1.
 CC Direct protein sequencing; Disease mutation; Glycoprotein; Hydrolase;
 CC lipid degradation; Polymorphism; Signal.
 CC SIGNAL 1 21
 CC CHAIN 22 441 Platelet-activating factor
 FT ACT_SITE 273 273 acetylhydrolase.
 FT ACT_SITE 296 296 Charge relay system.
 FT ACT_SITE 351 351 Charge relay system.
 FT CARBOHYD 423 423 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 433 433 N-linked (GlcNAc...)
 FT VARIANT 92 92 R -> H (common polymorphism;
 FT dbSNP:1805017).
 FT VARIANT 198 198 dbSNP:VAR_011583.
 FT I -> T (Common polymorphism;
 FT dbSNP:1805018).
 FT VARIANT 279 279 dbSNP:VAR_011584.
 FT V -> F (in PLA2G7 deficiency; loss of
 FT function; more common among Japanese than
 FT in Caucasians; risk factor for coronary
 FT artery disease and stroke).
 FT VARIANT 281 281 /FTId=VAR_004268.
 FT Q -> R (in PLA2G7 deficiency; loss of
 FT function).
 FT VARIANT 379 379 /FTId=VAR_011585.
 FT V -> A (Common polymorphism;
 FT dbSNP:1051931).
 FT VARIANT 108 108 /FTId=VAR_011586.
 FT S -> A: Activity is higher than wild type.
 FT S -> A: Loss of activity.
 FT D -> A: Almost no activity.
 FT D -> N: Diminished activity.
 FT D -> A: Loss of activity.
 FT D -> N: Loss of activity.
 FT D -> A: No change in activity.
 FT D -> A: Activity is higher than wild type.
 FT H -> A: Loss of activity.
 SQ SEQUENCE 441 AA; 50077 MW; 3BA9EEA9E8094A57 CRC64;
 Query Match 99.8%; Score 2354; DB 1; Length 441;
 Best Local Similarity 99.8%; Pred. No. 1.3e-174;

Matches 440; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MVPKHLVFLCGLAVVYDFDQYINPVAMKSSAWNKIQVLMAAASFGQTKIPRGN 60
Db 1 MVPKHLVFLCGLAVVYDFDQYINPVAMKSSAWNKIQVLMAAASFGQTKIPRGN 60

Qy 61 GPYSVGCTDLMDFTNKGTFRLRYPSQDNDRLDTLWIPNKEYFWGLSKFLGTHLWGN 120
Db 61 GPYSVGCTDLMDFTNKGTFRLRYPSQDNDRLDTLWIPNKEYFWGLSKFLGTHLWGN 120

Qy 121 LRLFGSMTPPANWNSPLRPGKEKYPVVFVSHGLGAFRTLYSAIGIDLASHGFIIVAAVEHR 180
Db 121 LRLFGSMTPPANWNSPLRPGKEKYPVVFVSHGLGAFRTLYSAIGIDLASHGFIIVAAVEHR 180

Qy 181 DRSASATYFKDQSAAEIGDKSWLYLRTLKQEEETHIRNEQVORAKESQALSILID 240
Db 181 DRSASATYFKDQSAAEIGDKSWLYLRTLKQEEETHIRNEQVORAKESQALSILID 240

Qy 241 HGKPVKNALDLKFDMEQLKDSIDREKTAIVGHSFGGATVIOTLSEDFRCGIALDAMF 300
Db 241 HGKPVKNALDLKFDMEQLKDSIDREKTAIVGHSFGGATVIOTLSEDFRCGIALDAMF 300

Qy 301 PLGDEVYSRIPOPLFFINSEYFQYIPANIIKMKKCYSPDKERKMITIRGSHVQNFADTF 360
Db 301 PLGDEVYSRIPOPLFFINSEYFQYIPANIIKMKKCYSPDKERKMITIRGSHVQNFADTF 360

Qy 361 TGKIIIGHMLKLGKGDIDSNAAIDLSNKASLAFLOKHLGLHKDFDQWDCLEGGDENLIPGT 420
Db 361 TGKIIIGHMLKLGKGDIDSNAAIDLSNKASLAFLOKHLGLHKDFDQWDCLEGGDENLIPGT 420

Qy 421 NINTNQHIMLQNSGIEKYN 441
Db 421 NINTNQHIMLQNSGIEKYN 441

RESULT 2

PAPA_BOVIN
ID PAPA_BOVIN STANDARD; PRT; 444 AA.
AC Q28017;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Platelet-activating factor acetylhydrolase precursor (EC 3.1.1.47)
DE (PAP acetylhydrolase) (PAP 2-acetylhydrolase) (LDL-associated phospholipase A2) (LDL-PLA(2)) (2-acetyl-1-alkylglycerophosphocholine esterase) (1-alkyl-2-acetyl-1-alkylglycerophosphocholine esterase).
GN Name=PLA2G7;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=96029630; PubMed=7592717; DOI=10.1074/jbc.270.43.25481;
RA Toelker L.W., Eberhardt C., Unger J., Trong H.L., Zimmermann G.A., McIntyre T.M., Stafforini D.M., Prescott S.M., Gray P.W.;
RT "Plasma platelet-activating factor acetylhydrolase is a secreted phospholipase A2 with a catalytic triad";
RL J. Biol. Chem. 270:25481-25487(1995).
CC -!- FUNCTION: Modulates the action of platelet-activating factor (PAP) by hydrolyzing the sn-2 ester bond to yield the biologically inactive lyso-PAP. Has a specificity for substrates with a short residue at the sn-2 position. It is inactive against long-chain phospholipids.
CC -!- CATALYTIC ACTIVITY: 1-alkyl-2-acetyl-sn-glycero-3-phosphocholine + H2O = 1-alkyl-sn-glycero-3-phosphocholine + acetate.
CC -!- SUBCELLULAR LOCATION: Extracellular.
CC -!- TISSUE SPECIFICITY: Plasma.
CC -!- SIMILARITY: Belongs to the AB hydrolase superfamily. Lipase family.

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EMBL; U34247; AAC48483.1; -;
DR InterPro; IPR008262; Lipase AS.
DR InterPro; IPR005065; PAF Ac hydrolase II.
DR InterPro; IPR000379; Ser_estra.
DR Pfam; PF03403; PAF-AH_P_I; 1.
DR PROSITE; PS00120; LIPASE_SER; 1.
KW Glycoprotein; Hydrolase; Lipid degradation; Signal.
FT SIGNAL 1 21 By similarity.
FT CHAIN 22 444 Platelet-activating factor acetylhydrolase.
FT ACT_SITE 274 274 Charge relay system (By similarity).
FT ACT_SITE 297 297 Charge relay system (By similarity).
FT ACT_SITE 352 352 Charge relay system (By similarity).
FT CARBOHYD 60 60 N-linked (GlcNAc...) (potential).
FT CARBOHYD 200 200 N-linked (GlcNAc...) (potential).
FT CARBOHYD 424 424 N-linked (GlcNAc...) (potential).
FT CARBOHYD 434 434 N-linked (GlcNAc...) (potential).
SQ SEQUENCE 444 AA; 50133 MW; 97689917BE2F4C38 CRC64;

Query Match 83.3%; Score 1964.5; DB 1; Length 444;
Best Local Similarity 82.4%; Pred. No. 2.6e-144;
Matches 364; Conservative 39; Mismatches 38; Indels 1; Gaps 1;

Qy 1 MVPKHLVFLCGLAVVYDFDQYINPVAMKSSAWNKIQVLMAAASFGQTKIPRGN 60
Db 1 MLPKSHALFCLCTCLALVYDFDQYINPVAMKSSAWNKIQVLMAAASFGQTKIPRGN 60

Qy 61 GPYSVGCTDLMDFTNKGTFRLRYPSQDNDRLDTLWIPNKEYFWGLSKFLGTHLWGN 120
Db 61 GPYSVGCTDLMDFTNKGTFRLRYPSQDNDRLDTLWIPNKEYFWGLSKFLGTHLWGN 120

Qy 121 LRLFGSMTPPANWNSPLRPGKEKYPVVFVSHGLGAFRTLYSAIGIDLASHGFIIVAAVEHR 180
Db 121 MGLFPGSMTPPANWNSPLRPGKEKYPVVFVSHGLGAFRTLYSAIGIDLASHGFIIVAAVEHR 180

Qy 181 DRSASATYFKDQSAAEIGDKSWLYLRTLKQEEETHIRNEQVORAKESQALSILID 239
Db 181 DGSASATYFKDQSAAEIGDKSWLYLRTLKQEEETHIRNEQVORAKESQALSILID 240

Qy 240 DHGKPVKNALDLKFDMEQLKDSIDREKTAIVGHSFGGATVIOTLSEDFRCGIALDAMF 299
Db 241 DHGKPVKNALDLKFDMEQLKDSIDREKTAIVGHSFGGATVIOTLSEDFRCGIALDAMF 300

Qy 300 PPLGDEVYSRIPOPLFFINSEYFQYIPANIIKMKKCYSPDKERKMITIRGSHVQNFADTF 359
Db 301 PPLGDEVYSRIPOPLFFINSEYFQYIPANIIKMKKCYSPDKERKMITIRGSHVQNFADTF 360

Qy 360 ATGKIIGHMLKLGKGDIDSNAAIDLSNKASLAFLOKHLGLHKDFDQWDCLEGGDENLIPG 419
Db 361 ATGKIIGHMLKLGKGDIDSNAAIDLSNKASLAFLOKHLGLHKDFDQWDCLEGGDENLIPG 420

Qy 420 TNINTNQHIMLQNSGIEKYN 441
Db 421 TNINTNQHIMLQNSGIEKYN 442

RESULT 3

PAPA_CANFA
ID PAPA_CANFA STANDARD; PRT; 444 AA.
AC Q28262;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Platelet-activating factor acetylhydrolase precursor (EC 3.1.1.47)
DE (PAP acetylhydrolase) (PAP 2-acetylhydrolase) (LDL-associated

phospholipase A2) (LDL-PLA(2)) (2-acetyl-1-alkylglycerophosphocholine esterases) (1-alkyl-2-acetyl-1-alkylglycerophosphocholine esterases).

Name=PLA2G7;
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Splice;
 RX MEDLINE=96029630; PubMed=7592717; DOI=10.1074/jbc.270.43.25481;
 RA Tjoelker L.W., Eberhardt C., Unger J., Trong H.L., Zimmerman G.A.,
 RA McIntyre T.M., Stafforini D.M., Prescott S.M., Gray P.W.;
 RT "Plasma platelet-activating factor acetylhydrolase is a secreted
 phospholipase A2 with a catalytic triad.";
 RL J. Biol. Chem. 270:25481-25487 (1995).
 CC -1- FUNCTION: Modulates the action of platelet-activating factor (PAF)
 CC by hydrolyzing the sn-2 ester bond to yield the biologically
 CC inactive lyso-PAF. Has a specificity for substrates with a short
 CC residue at the sn-2 position. It is inactive against long-chain
 CC phospholipids.
 CC -1- CATALYTIC ACTIVITY: 1-alkyl-2-acetyl-sn-glycero-3-phosphocholine +
 CC H(2)O = 1-alkyl-sn-glycero-3-phosphocholine + acetate.
 CC -1- SUBCELLULAR LOCATION: Extracellular.
 CC -1- TISSUE SPECIFICITY: Plasma.
 CC -1- SIMILARITY: Belongs to the AB hydrolase superfamily. Lipase
 CC family.
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EMBL; U34246; AAC48484.1; -;
 DR InterPro; IPR008262; Lipase_AS.
 DR InterPro; IPR005065; PAF_Ac_Hydrolp_II.
 DR InterPro; IPR000379; Ser_estra.
 DR Pfam; PF03403; PAF-AH_P_II; 1.
 DR PROSITE; PS00120; LIPASE_SER; 1.
 KW Glycoprotein; Hydrolase; Lipid degradation; Signal.
 FT SIGNAL 1 21 By similarity.
 FT CHAIN 22 444 Platelet-activating factor acetylhydrolase.
 FT ACT_SITE 274 Charge relay system (By similarity).
 FT ACT_SITE 297 Charge relay system (By similarity).
 FT ACT_SITE 352 Charge relay system (By similarity).
 FT CARBOHYD 60 N-linked (GlcNAc...) (potential).
 FT CARBOHYD 200 N-linked (GlcNAc...) (potential).
 FT CARBOHYD 424 N-linked (GlcNAc...) (potential).
 SQ SEQUENCE 444 AA; 50136 MW; 814EF0AE38B0744AC CRC64;

Query Match 82.18; Score 1935.5; DB 1; Length 444;
 Best Local Similarity 80.8; Pred. No. 4.7e-142;
 Matches 357; Conservative 38; Mismatches 46; Indels 1; Gaps 1;

QY 1 MVPPKHLVFLCGLAVVYFQWQYINPVVHKKSSAWNKKIOVLMAAASFGQTKIPRG 60
 DB 1 MLPPKHALFLCSCSLTLVHPDQDLNPVHVRSSAWANKIQALMAAASIRSRPKGN 60
 QY 61 GPVSVGCTDLMPHTNKGTLRLRYPSQDNDRLTLWIPNKEYFWGLSKFLGTHWLMGNI 120
 DB 61 GSVSVGCTDLMPDYNKGTFLRLYPSQEDDHSDDLWIPNKEYFWGLSKFLGTHWLMGKI 120
 QY 121 LRLFLGSMWTPANWNSPLRCEKYPVLFVSHGIGAPETLYSAIGIDIASHGFTVAVEHR 180
 DB 121 LSFEGSVTPPANWNSPLRCEKYPVLFVSHGIGAPETLYSAIGIDIASHGFTVAIEHR 180
 QY 181 DRASATYFFKDSAAEIGDKSWLYLRLTKQ-BEETHIRNEQVRQAKESQALSILDI 239
 DB 181 DGSATYFFKDSAAEIGNKNSWLYLQLAPGDEIHRNEQVRQAKESQALNLLDI 240

QY 240 DHGKPVKNALDLKPFDMQKDSIDREKIAVIGHSFGGATVIQTLSEDFRCGIALDAWM 299
 DB 241 DHGKPIKNVLDLDFDVEQLKDSIDRDKIAVIGHSFGGATVLQALSEDFRCGIALDAWM 300
 QY 300 FPLGDEVYSRIPQPLPFINSEYQYPAIIKMKKCYSPDKERKMITTIGSVHQNFADFTF 359
 DB 301 LPLDDAIYSRIPQPLPFINSEYQYPAIIKMKKCYSPDKERKMITTIGSVHQNFADFTF 360
 QY 360 ATGKIGHMLKLGKGDIDSNAAIDLSNKAFLQKHLGHKDFQDQWCLLEGDDENLIPG 419
 DB 361 TTGKIVGYITFLKGDIDSNVAIDLCKASLAFLQKHLGLRKFQDQWDSLIEGKDNLMFG 420
 QY 420 TNINTTNOHIMLQNSGIEKYN 441
 DB 421 TNINTTNEHDTLQNSPEAKSN 442

RESULT 4
 PAF_A CAVPO STANDARD; PRT; 436 AA.
 AC P70683;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Platelet-activating factor acetylhydrolase precursor (EC 3.1.1.47)
 DE (PAF acetylhydrolase) (PAF 2-acetylhydrolase) (LDL-associated
 DE phospholipase A2) (LDL-PLA(2)) (2-acetyl-1-alkylglycerophosphocholine
 DE esterase) (1-alkyl-2-acetyl-1-alkylglycerophosphocholine esterases).
 GN Name=PLA2G7; Synonyms=PAFAH;
 OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
 OC NCBI_TaxID=10141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Hartley; TISSUE=Liver;
 RX MEDLINE=97103479; PubMed=8947850;
 RA Karasawa K., Kuge O., Kawasaki K., Nishijima M., Nakano Y., Tomita M.,
 RA Yokoyama K., Setaka M., Nojima S.;
 RT "Cloning, expression and characterization of plasma platelet-
 RT activating factor-acetylhydrolase from guinea pig.";
 RL J. Biochem. 120:838-844 (1996).
 CC -1- FUNCTION: Modulates the action of platelet-activating factor (PAF)
 CC by hydrolyzing the sn-2 ester bond to yield the biologically
 CC inactive lyso-PAF. Has a specificity for substrates with a short
 CC residue at the sn-2 position. It is inactive against long-chain
 CC phospholipids.
 CC -1- CATALYTIC ACTIVITY: 1-alkyl-2-acetyl-sn-glycero-3-phosphocholine +
 CC H(2)O = 1-alkyl-sn-glycero-3-phosphocholine + acetate.
 CC -1- SUBCELLULAR LOCATION: Extracellular.
 CC -1- TISSUE SPECIFICITY: Plasma.
 CC -1- SIMILARITY: Belongs to the AB hydrolase superfamily. Lipase
 CC family.
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EMBL; D67037; BAAL1054.1; -;
 DR PIR; JC5021; JC5021.
 DR InterPro; IPR008262; Lipase_AS.
 DR InterPro; IPR005065; PAF_Ac_Hydrolp_II.
 DR InterPro; IPR000379; Ser_estra.
 DR Pfam; PF03403; PAF-AH_P_II; 1.
 DR PROSITE; PS00120; LIPASE_SER; 1.
 KW Glycoprotein; Hydrolase; Lipid degradation; Signal.
 FT SIGNAL 1 21 By similarity.
 FT CHAIN 22 436 Platelet-activating factor

FT ACT_SITE 271 acetylhydrolase.
 FT ACT_SITE 294 Charge relay system (By similarity).
 FT ACT_SITE 349 Charge relay system (By similarity).
 FT CARBOHYD 76 N-linked (GlcNAc...) (potential).
 FT CARBOHYD 200 N-linked (GlcNAc...) (potential).
 FT CARBOHYD 324 N-linked (GlcNAc...) (potential).
 SQ SEQUENCE 436 AA; 49062 MW; C359D96B392FEE11 CRC64;

Query Match 66.7%; Score 1572.5; DB 1; Length 436;
 Best Local Similarity 66.2%; Pred. No. 8.1e-114;
 Matches 292; Conservative 63; Mismatches 79; Indels 7; Gaps 2;

Qy 1 MYPKLVHLCCLAVVYPPDQYINPVAHMKSSAWNKIOVLMAAASFGQTKIPRGN 60
 Db 1 MAPPKLHTLFCSLGFLVHPDWRDLDPVYIOSSVNIQIOSELLITSFGHTTIPKGN 60
 Qy 61 GPYSVGCTDLMFDRHTNKGTFRLRYPPSQDNDRLTLMPNKEYFWGLSKFLGTHLWLMGNI 120
 Db 61 GPYSVGCTDLMSGYTNQSSFLRLYPPSQDNDPDPALMIPNEYFQGLTEILGASSFLGKL 120
 Qy 121 LRLFGSMTPPANWNSPLRPGEXPLVVFVSHGLGAFRTLYSAIGIDLASHGFIVAIVEHR 180
 Db 121 LKLLYGVKVPKWNPLKTEGKPLIIFSHGLGAFRTLYSAIGIDLASHGFIVAIVEHR 180
 Qy 181 DRASATYYPKQSAAEIGDKSWLYLRLTKQEBETHIRNEQVORAKESQALSLLIDID 240
 Db 181 DESAATYYPQDAPAESGNRSWYIKV--GNLSETEERKQLRQRBECQALSLLSID 238
 Qy 241 HGKPVKNALDKFDMEQLKDSIDREKIAVIGHSGFGGATVIQTLSEDRFRFCGIALDAWMF 300
 Db 239 EGEFVKVLDLNFIDIQKGLSKVKAIIIGHSGFGGATVIQTLSEDRFRFCGIALDPWMP 298
 Qy 301 PLGDEVYSRIPOPLFFINSEYFQYPANIIKMKCYSPDKERKMITIRGSHQNFADFTFA 360
 Db 299 PVGEDVHSKIPOPLFFINSEYFQSAANDTKIEKYPQKERKMITAVKGVSHNFPVDTFA 358
 Qy 361 TGKLIIGHMLKLGIDNSAIDLSNKASLAFLOKHGLGHKDFDQWDCLEGGDENLIPGT 420
 Db 359 TGKLIIGHMLKLGIDNSAIDLSNKASLAFLOKHGLGHKDFDQWDCLEGGDENLIPGT 418
 Qy 421 NINTNQHIMLQNSSGIEKYN 441
 Db 419 TIPT-----MQSSTGTGEQRN 434

RESULT 5
 Q921T4
 ID Q921T4 PRELIMINARY; PRT; 440 AA.
 AC Q921T4
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Phospholipase A2, group VII (Platelet-activating factor
 DE acetylhydrolase, plasma).
 GN Name=Pla2g7;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan B., Moore T., Max S.I., Wang J., Heish F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bobak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,
 RA Fahney J., Helton E., Kettelman M., Madan A.C., Rodrigues S., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
 RA Straubeberg R.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC010726; AAH10726.1; -;
 DR MGD; MGI:1351327; Pla2g7.
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR GO; GO:0006954; P:inflammatory response; TAS.
 DR Pfam; PF03403; PAF-AH_P_II; 1.
 DR PROSITE; PS00120; LIPASE_SER; UNKNOWN_1.
 KW Hydrolase.
 SQ SEQUENCE 440 AA; 49230 MW; 17C8B4D28F085794 CRC64;

Query Match 66.0%; Score 1556.5; DB 2; Length 440;
 Best Local Similarity 67.1%; Pred. No. 1.4e-112;
 Matches 296; Conservative 55; Mismatches 89; Indels 1; Gaps 1;

Qy 1 MYPKLVHLCCLAVVYPPDQYINPVAHMKSSAWNKIOVLMAAASFGQTKIPRGN 60
 Db 1 MVLKQLALFCLLCCLPWHPFHQDTSSP-DFRPSPVHFHLQSWMAASGHSKIPKGN 59
 Qy 61 GPYSVGCTDLMFDRHTNKGTFRLRYPPSQDNDRLTLMPNKEYFWGLSKFLGTHLWLMGNI 120
 Db 60 GSYFVGCTDLMFVGVNESVFRVLYYPAQDQGRDLTVMPNKEYFLGLSIFLGTSPISVNI 119
 Qy 121 LRLFGSMTPPANWNSPLRPGEXPLVVFVSHGLGAFRTLYSAIGIDLASHGFIVAIVEHR 180
 Db 120 LHLVLSLTTPAGWNSPLRTGEXPLVVFVSHGLGAFRTLYSAIGIDLASHGFIVAIVEHR 179
 Qy 181 DRASATYYPKQSAAEIGDKSWLYLRLTKQEBETHIRNEQVORAKESQALSLLIDID 240
 Db 180 DRASATYYPFEDQVAAKVENRWLYLKVQKQESSEVRKEQVQORALECSRALSLIDIE 239
 Qy 241 HGKPVKNALDKFDMEQLKDSIDREKIAVIGHSGFGGATVIQTLSEDRFRFCGIALDAWMF 300
 Db 240 HGDPKENVLGSADFMDKQLKDAIDETKIALMGHSGFGGATVLQALSEDRFRFCGVALDPWY 299
 Qy 301 PLGDEVYSRIPOPLFFINSEYFQYPANIIKMKCYSPDKERKMITIRGSHQNFADFTFA 360
 Db 300 PVNEELYSRTLOPLFFINSAKFTQPKDIAMKKFYQPKERKMITIRGSHQNFDDFTFV 359
 Qy 361 TGKLIIGHMLKLGIDNSAIDLSNKASLAFLOKHGLGHKDFDQWDCLEGGDENLIPGT 420
 Db 360 TGKLIIGHMLKLGIDNSAIDLSNKASLAFLOKHGLGHKDFDQWDCLEGGDENLIPGS 419
 Qy 421 NINTNQHIMLQNSSGIEKYN 441
 Db 420 PFDAVTAQPAQHSPGSGTQN 440

RESULT 6
 Q8BK03
 ID Q8BK03 PRELIMINARY; PRT; 440 AA.
 AC Q8BK03
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Mus musculus 12 days embryo spinal ganglion cDNA, RIKEN full-length
 DE enriched library, clone:DI30049018 product:phospholipase A2 group VII
 DE (platelet-activating factor acetylhydrolase, plasma), full insert
 DE sequence.


```

CC CC -|- SUBCELLULAR LOCATION: Extracellular.
CC CC -|- TISSUE SPECIFICITY: Plasma.
CC CC -|- SIMILARITY: Belongs to the AB hydrolase superfamily. Lipase
CC CC family.
CC CC -----
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CC CC or send an email to license@isb-sib.ch).
CC CC -----
CC CC EMBL; U34277; AAC52274.1; -.
CC CC MGD; MGI:1351327; Pla2g7.
CC CC InterPro; IPR008262; Lipase AS.
CC CC InterPro; IPR005065; PAF Ac hydrolip II.
CC CC InterPro; IPR000379; Ser_eatrs.
CC CC Pfam; PF03403; PAF-AH_P_II; 1.
CC CC PROSITE; PS00120; LIPASE_SER; 1.
CC CC Glycoprotein; Hydrolase; Lipid degradation; Signal.
CC CC SIGNAL 1 21 By similarity.
CC CC CHAIN 22 440 Platelet-activating factor
CC CC acetylhydrolase.
CC CC ACT_SITE 272 272 Charge relay system (By similarity).
CC CC ACT_SITE 295 295 Charge relay system (By similarity).
CC CC ACT_SITE 350 350 Charge relay system (By similarity).
CC CC CARBOHYD 59 59 N-linked (GlcNAc...) (potential).
CC CC CARBOHYD 75 75 N-linked (GlcNAc...) (potential).
CC CC CARBOHYD 199 199 N-linked (GlcNAc...) (potential).
CC CC SEQUENCE 440 AA; 49361 MW; C82A68AD42F482EB CRC64;
CC CC
CC CC Query Match 64.2%; Score 1514.5; DB 1; Length 440;
CC CC Best Local Similarity 65.8%; Pred. No. 2.7e-109;
CC CC Matches 290; Conservative 55; Mismatches 95; Indels 1; Gaps 1;
CC CC
CC CC Qy 1 MVPLKLVHLCCLAVYFPDQYINPVAMKSSAWNKIQVMAASFGQTKIPRGN 60
CC CC Db 1 MVPLKQALQALFCLCLPWFHPFHQDTSSF-DPRPSVNFPHKQSVMAAGSGHSKIPKGN 59
CC CC
CC CC Qy 61 GPYSVGCTDLDFHNTKGTFLRLVYPSQDNDRLDTLTPNKEYFWGLSKPLGTHLMAGNI 120
CC CC Db 60 GSYVPVGTDLDFGNGSVFRLVYPPAQDQRLDTVTPNKEYFLGLSIFLGTSPVGN 119
CC CC
CC CC Qy 121 LRLFLGSMTPANNNSPLRPGCKYPLVVFSHGLGAFRTLYSAIGIDLASHGFIVAIVEHR 180
CC CC Db 120 LHLLYGSLTTPASWNSPLRTGCKYPLVVFSHGLGAFRTLYSAIGLASNGFIVATVEHR 179
CC CC
CC CC Qy 181 DRASATYFKDQAAEIGDKSWLYRLTKQEBETHINNEQVQRRAKCEQSALSLILDID 240
CC CC Db 180 DRASATYFFEDQVAAKVNNRSMWLYLRKVQOESESVRKEQVQORAIETCSRLSAILDIE 239
CC CC
CC CC Qy 241 HGKPVKVALDLKPDMEQLKDSIDREKTAIVGHSGFGATVITLSEDFRCGIALDAWVF 300
CC CC Db 240 HGDPKENVLGSADFDMKQKDAIDETKALMGHSGFGATVQLQALSDQRFRCGVALDPWY 299
CC CC
CC CC Qy 301 PLGDEVYSRIPQLFFINSEYFQYPANIIRMKKCYSPDKRKMITIRGSHVQNFADPTFA 360
CC CC Db 300 PVNEELYSRTIQLPLLFINSKAFQTPKDIAMKKFYQDPKERNQYQGLRHFQDFTFV 359
CC CC
CC CC Qy 361 TGIIGHMLKUKGIDSDNAIDLNKASLAFLOKHLGLHKDFDQWDCLIEGDDENLIPGT 420
CC CC Db 360 TGIIGNKLTKGETSDRVAIDLTKASMAFLQKHLGLQKDFDQWDPLVEGDDENLIPGS 419
CC CC
CC CC Qy 421 NINTTNHIMLQNSGIEKYN 441
CC CC Db 420 PFDVATQAPAOQHSPGSGTON 440
CC CC
CC CC RESULT 8
CC CC Q9DB74 PRELIMINARY; PRT; 346 AA.
CC CC AC Q9DB74;

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DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus adult male cerebellum cDNA, RIKEN full-length enriched
DE library, clone:1500005E13 product:phospholipase A2 group VII
DE (platelet-activating factor acetylhydrolase, plasma), full insert
DE sequence.
GN Name=Pla2g7;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=9279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RA The FANTOM Consortium;
RT the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imoto K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shingawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RT Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RL EMBL; AK005158; BAB23849.1; -.
DR

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DR MGD; MGI:1351327; Pla2g7.
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR GO; GO:0006954; P:inflammatory response; TAS.
 DR InterPro; IPR009262; Lipase AS.
 DR InterPro; IPR005065; PAF_Ac_hydrolase II.
 DR InterPro; IPR000379; Ser_estr.
 DR Pfam; PF03403; PAF-AH_P_II; 1.
 DR PROSITE; PS00120; LIPASE_SER; UNKNOWN_1.
 KW Hydrolase.
 SQ SEQUENCE 346 AA; 38967 MW; D68A2A128402E554 CRC64;

Query Match 52.0%; Score 1226.5; DB 2; Length 346;
 Best Local Similarity 66.9%; Pred. No. 5e-87;
 Matches 232; Conservative 46; Mismatches 68; Indels 1; Gaps 1;

QY 1 MYPKLVHFLCCLAVVYFEDQYINPVAMKSSAWNKKIQLVMAASFGQTKIPRGN 60
 DB 1 MVLKLAQLFCLLCCLPWFHFFHWDTSPP-DFRPSVNFHKLQSVMAAGSHKIPRGN 59
 QY 61 GPYSVGCTDLMDHFNKGTFLRLYPPSQDRLDLMIPNKEYFWGLSKFLGTHLWMGNI 120
 DB 60 GSYVPGCTDLDFMGYGNESVFLRLYPPAQDQGLDLMIPNKEYFLGLSIFLGTSPVIGNI 119
 QY 121 LRLFLGSMTPANWNSPLRGEKYPVLVFSHGLGAFRTLYSAIGIDLAHGFVAIVEHR 180
 DB 120 LHLLYGSLTTPASWNSPLRGEKYPVLVFSHGLGAFRTLYSAIGIDLAHGFVAIVEHR 179
 QY 181 DRASATYFQKDSAAIGDKSMLYLRKQEEETHIRNEQVRORAKECSOALSLLIDID 240
 DB 180 DRASATYFQKDSAAIGDKSMLYLRKQEEETHIRNEQVRORAKECSOALSLLIDID 239
 QY 241 HGKPVKNALDKFDMELKDSIDREKIAVIGHSGFGGATVIQTLSQDQRFRCGIALDAWFM 300
 DB 240 HGDPKENVLSAFDMKQLKDAIDETKIALMGHSGFGGATVIQTLSQDQRFRCGIALDAWFM 299
 QY 301 PLGDEVYSRTPQLFFNSFYQYPANIIKMKCYSPDKKRMITIR 347
 DB 300 FVNEELYSRTQLPLLFINSFAKFPQPKDIAMKKFYQPKDKRMITIK 346

RESULT 9
 PAPA CHICK
 ID "PAPA_CHICK STANDARD; PRT; 422 AA.
 AC Q90678;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Platelet-activating factor acetylhydrolase precursor (EC 3.1.1.47)
 DE (PAF acetylhydrolase) (PAF 2-acylhydrolase) (LDL-associated
 DE phospholipase A2) (LDL-PLA(2)) (2-acetyl-1-alkylglycerophosphocholine
 DE esterase) (1-alkyl-2-acetyl-1-alkylglycerophosphocholine esterase).
 GN Name=PLA2G7;
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen.
 RX MEDLINE=96029630; PubMed=7592717; DOI=10.1074/jbc.270.43.25481;
 RA Tjoelker L.W., Eberhardt C., Unger J., Trong H.L., Zimmerman G.A.,
 RA McIntyre T.M., Staforini D.M., Prescott S.M., Gray P.W.;
 RT "Plasma platelet-activating factor acetylhydrolase is a secreted
 RT phospholipase A2 with a catalytic triad";
 RL J. Biol. Chem. 270:25481-25487(1995).
 CC -1- FUNCTION: Modulates the action of platelet-activating factor (PAF)
 CC by hydrolyzing the sn-2 ester bond to yield the biologically
 CC inactive lyso-PAF. Has a specificity for substrates with a short
 CC residue at the sn-2 position. It is inactive against long-chain
 CC phospholipids.
 CC -1- CATALYTIC ACTIVITY: 1-alkyl-2-acetyl-sn-glycero-3-phosphocholine +
 CC H2O = 1-alkyl-sn-glycero-3-phosphocholine + acetate.

CC -1- SUBCELLULAR LOCATION: Extracellular.
 CC -1- TISSUE SPECIFICITY: Plasma.
 CC -1- SIMILARITY: Belongs to the AB hydrolase superfamily. Lipase
 CC family.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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 CC
 CC ENBL; U34278; AAC59717.1; -
 DR InterPro; IPR008262; Lipase AS.
 DR InterPro; IPR005065; PAF_Ac_hydrolase II.
 DR InterPro; IPR000379; Ser_estr.
 DR Pfam; PF03403; PAF-AH_P_II; 1.
 DR PROSITE; PS00120; LIPASE_SER; 1.
 KW Glycoprotein; Hydrolase; Lipid degradation; Signal.
 FT SIGNAL 1 21 By similarity.
 FT CHAIN 22 422 Platelet-activating factor
 FT acetylhydrolase.
 FT ACT_SITE 266 266 Charge relay system (By similarity).
 FT ACT_SITE 289 289 Charge relay system (By similarity).
 FT ACT_SITE 345 345 Charge relay system (By similarity).
 FT CARBOHYD 331 331 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 422 AA; 47046 MW; 15A5C794376E9141 CRC64;

Query Match 48.0%; Score 1131.5; DB 1; Length 422;
 Best Local Similarity 55.3%; Pred. No. 1.6e-96;
 Matches 230; Conservative 63; Mismatches 99; Indels 27; Gaps 7;

QY 35 SSAWNKIOVLV-----AAASFGQ-----TKIPRGNPYSVGCTDLMDHFNKNG 78
 DB 2 ASLVVARRVFMKSRASGSASAKAATMGSGGAEKGYRIPAGKGPVAVGCTDLMDGDAEG 61
 QY 79 TFLRLYPPS-QDNDRLDLMIPNKEYFWGLSKFLGTHLWMG-NILRLFGSMTPANWNS 136
 DB 62 SFRLYVLSGDDTDTEETWIPDKKEYVQGLSDFLNVVRLGRLVQYVGVSVTCAPKSA 121
 QY 137 PLRPGKYPVLVFSHGLGAFRTLYSAIGIDLAHGFVAIVEHRDRSASATYFQKDSAA 196
 DB 122 AFKPGSKYPLLVFSHGLGAFRTLYSAIGIDLAHGFVAIVEHRDRSASATYFQKDSAA 181
 QY 197 EIG-----DKSWLYRLTKO-EEETHIRNEQVRORAKECSOALSLLIDIDHGKPVKNA 248
 DB 182 EPEDQTSVGKEWYIYRKLAGEEERCLRHQVQQAQECIKALNLLKISSGEFWMV 241
 QY 249 LDLKFDMEQLKDSIDREKIAVIGHSGFGGATVIQTLSQDQRFRCGIALDAWFMFLGDEVY- 307
 DB 242 LNSDFDWNHLKDSVDTSRIVAMGHSGFGGATVIESLSKEIRFRFCGIALDAWMLPVGDDTYQ 301
 QY 308 SRTPQLFPINSEYFQYPANIIKMKCYSPDKKRMITIRSGVHONFADFTPATKLIHG 367
 DB 302 SSYQQPLLFINSFAKFPQPKDIAMKKLSNDTNKMTITKSGVHQSPFDFTFVSGEILIG 361
 QY 368 MLKLKGDIDNSAIDLSNKAFLQKHLGLHDFQWDCLIEGDDENLIPGNIN 423
 DB 362 FFKLKGIDPNEAIDICNHSALFLQKHLGLHDFQWDCLIEGDDENLIPGNIN 417

RESULT 10
 Q6NYI7
 ID Q6NYI7 PRELIMINARY; PRT; 404 AA.
 AC Q6NYI7;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Zgc:77563.
 GN ORFNames=zgc:77563;
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

QY 57 PRGNPYSVGVCTDLMFDHTNKGTLRLYYPSQDNDRDL-TLWIPNKYFVGLSKFL--GT 113
 Db 10 PPSGPHHIGCTDVMGHSLEGLSFLRFLYPCASETCEQLWIPRYEYCVGLADLYQYNK 69
 QY 114 HMLMGNILRLFLGSMWTPPANWNSPLRPECK-YPLVVFESHGIGARTLYSAIGIDLASHGF 172
 Db 70 RW-VGLLFNVGIGSRLPVSWMGPKTESGYPIIILSHGLGGRVSVSAFCMELASRGF 128
 QY 173 IVAAVEHRDRSASATYFFK-----DQSAAEIGDKSWLYRLTKQ-EEETHIRNEQVORAK 227
 Db 129 VVAIEHRDQSAATYFCKQTSQSSSTESLEEWIPFRRIKEGEKEFHVRNPQVHORAK 188
 QY 228 ECSQALSILIDHKGKPVKNALDLKFDMEQLKOSIDREKIAVIGHSGFGATVITQISEDQ 287
 Db 189 ECVRLVQLQDASAGKPVINVPFGGLDLMTLTKGSDMSRVAVMHSFGGATAILALQDEA 248
 QY 288 RFRGCIADLAWMFPGLGDEVYSRIPQPLFFINSEYFQYPAIIKMKCYSPDKERKMITIR 347
 Db 249 QFRCAIALDAMWPFLEHDFYFKARGPVFFINVEKFTQVESVNLMMKKICAQHEQSRIVTVL 308
 QY 348 GSVHQNFADEFTATGKIIGHMLK--LKGDIDSNAAIDLSNKAFLQKHLGLHDKPQDQW 405
 Db 309 GAVHRSQTDFAFVTGNMIGKLFSSGTRGTLDPYSGQEVVMVRAFLQKHLGLHDKPQDQW 368
 QY 406 DCLIEGDDENLIPG 419
 Db 369 NSFIEGIGPSLIQ 382

RESULT 12

PAF2_MOUSE
 ID PAF2_MOUSE STANDARD; PRT; 390 AA.
 AC Q8VDG7; Q8R0V7;
 DT 25-OCT-2004 (Rel. 45, Created)
 DT 25-OCT-2004 (Rel. 45, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Platelet-activating factor acetylhydrolase 2, cytoplasmic
 DE (EC 3.1.1.47) (Serine dependent phospholipase A2).
 GN Mus musculus (Mouse).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Liver, and Mammary gland;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McWan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Vallalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
 RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- FUNCTION: Has a marked selectivity for phospholipids with short
 acyl chains at the sn-2 position. May share a common physiologic
 function with the plasma-type enzyme (By similarity).
 CC -1- CATALYTIC ACTIVITY: 1-alkyl-2-acetyl-sn-glycero-3-phosphocholine +
 H(2)O = 1-alkyl-sn-glycero-3-phosphocholine + acetate.

CC -1- SUBUNIT: Monomer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -1- SIMILARITY: Belongs to the serine esterase family.
 CC
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 entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC
 CC EMBL; BC021890; AAH21890.1; -
 DR EMBL; BC025495; AAH25495.1; -
 DR EMBL; BC025938; AAH25938.1; -
 DR MGI; MGI:2140321; Pafah2.
 DR InterPro; IPR008262; Lipase_AS.
 DR InterPro; IPR005065; PAF_AC_hydrol_II.
 DR InterPro; IPR000379; Ser_estrs.
 DR Pfam; PF03403; PAF-AH_P_II; 1.
 DR PROSITE; PS00120; LIPASE_SER; 1.
 DR Hydrolase; Lipid degradation.
 KW ACT_SITE 234 234 Charge relay system (By similarity).
 FT ACT_SITE 257 257 Charge relay system (By similarity).
 FT ACT_SITE 312 312 Charge relay system (By similarity).
 SQ SSEQUENCE 390 AA; 43465 MW; 12AF12PFF506ADE2 CRC64;
 Query Match 34.3%; Score 809; DB 1; Length 390;
 Best Local Similarity 43.6%; Pred. No. 18e-54;
 Matches 163; Conservative 72; Mismatches 127; Indels 12; Gaps 7;
 QY 57 PRGNPYSVGVCTDLMFDHTNKGTLRLYYPSQDNDRDL-TLWIPNKYFVGLSKFL--GT 113
 Db 10 PPSGPHHIGCTDVMGHSLEGLSFLRFLYPCASETCEQLWIPRYEYCVGLADLYQYNK 69
 QY 114 HMLMGNILRLFLGSMWTPPANWNSPLRPECK-YPLVVFESHGIGARTLYSAIGIDLASHGF 172
 Db 70 RW-VGLLFNVGIGSRLPVSWMGPKTESGYPIIILSHGLGGRVSVSAFCMELASRGF 128
 QY 173 IVAAVEHRDRSASATYFFK-----DQSAAEIGDKSWLYRLTKQ-EEETHIRNEQVORAK 227
 Db 129 VVAIEHRDQSAATYFCKQTSQSSSTESLEEWIPFRRIKEGEKEFHVRNPQVHORAK 188
 QY 228 ECSQALSILIDHKGKPVKNALDLKFDMEQLKOSIDREKIAVIGHSGFGATVITQISEDQ 287
 Db 189 ECVRLVQLQDASAGKPVINVPFGGLDLMTLTKGSDMSRVAVMHSFGGATAILALQDEA 248
 QY 288 RFRGCIADLAWMFPGLGDEVYSRIPQPLFFINSEYFQYPAIIKMKCYSPDKERKMITIR 347
 Db 249 QFRCAIALDAMWPFLEHDFYFKARGPVFFINVEKFTQVESVNLMMKKICAQHEQSRIVTVL 308
 QY 348 GSVHQNFADEFTATGKIIGHMLK--LKGDIDSNAAIDLSNKAFLQKHLGLHDKPQDQW 405
 Db 309 GAVHRSQTDFAFVTGNMIGKLFSSGTRGTLDPYSGQEVVMVRAFLQKHLGLHDKPQDQW 368
 QY 406 DCLIEGDDENLIPG 419
 Db 369 NSFIEGIGPSLIQ 382
 RESULT 13
 PAF2_HUMAN
 ID PAF2_HUMAN STANDARD; PRT; 392 AA.
 AC Q99487; O15458;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 28-OCT-2004 (Rel. 45, Last annotation update)
 DE Platelet-activating factor acetylhydrolase 2, cytoplasmic
 DE (EC 3.1.1.47) (Serine dependent phospholipase A2) (HSD-PLA2).
 GN Name=PAFAH2;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=97115847; PubMed=8955149; DOI=10.1074/jbc.271.51.33032;
 RA Hattori K., Adachi H., Matsuzawa A., Yamamoto K., Tsujimoto M.,
 RA Aoki J., Hattori M., Arai H., Inoue K.,
 RT "cDNA cloning and expression of intracellular platelet-activating
 RT factor (PAF) acetylhydrolase II. Its homology with plasma PAF
 RT acetylhydrolase.";
 RL Biochem. J. 330:1309-1315(1998).
 [2]
 RN SEQUENCE FROM N.A., SEQUENCE OF 1-5, AND MASS SPECTROMETRY.
 RC TISSUE=Prostate;
 RX MEDLINE=98161812; PubMed=9494101;
 RA Moore S.Q.J., Southern C., Boyd H.G., Terrett J.A., Macphee C.H.,
 RA Rices S.Q.J., Gloger I.S., Tew D.G.,
 RT "Expression, purification and characterization of a human serine-
 RT dependent phospholipase A2 with high specificity for oxidized
 RT phospholipids and platelet activating factor.";
 RL Biochem. J. 330:1309-1315(1998).
 [3]
 RN SEQUENCE FROM N.A.
 RC TISSUE=EYE;
 RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S.G., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Wozny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fanev J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [4]
 RP REVIEW
 RX MEDLINE=97364701; PubMed=9218411; DOI=10.1074/jbc.272.29.17895;
 RA Stafforini D.M., McIntyre T.M., Zimmerman G.A., Prescott S.M.,
 RT "Platelet-activating factor acetylhydrolases.";
 RL J. Biol. Chem. 272:17895-17898(1997).
 CC -1- FUNCTION: Has a marked selectivity for phospholipids with short
 CC acyl chains at the sn-2 position. May share a common physiologic
 CC function with the plasma-type enzyme.
 CC -1- CATALYTIC ACTIVITY: 1-alkyl-2-acetyl-sn-glycero-3-phosphocholine +
 CC H(2)O = 1-alkyl-sn-glycero-3-phosphocholine + acetate.
 CC -1- ENZYME REGULATION: Inhibited by phenylmethanesulfonyl fluoride,
 CC 3,4-dichloroisocoumarin, diisopropyl fluorophosphate (DPP) and
 CC diethyl p-nitrophenyl phosphate (DNP).
 CC -1- SUBUNIT: Monomer.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- TISSUE SPECIFICITY: Broadly expressed in different tissues, but
 CC high in B and T lymphocytes. In brain, expression is restricted to
 CC amygdala and frontal cortex.
 CC -1- MASS SPECTROMETRY: MW=44162; METHOD=Electrospray; RANGE=1-392;
 CC NOTE=Ref.2.
 CC -1- SIMILARITY: Belongs to the serine esterase family.

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
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 DR EMBL; D87845; BAA13468.1; -;
 DR EMBL; U89386; AAC39707.1; -;
 DR EMBL; BC001158; AA01158.1; -;
 DR Genew; HGNC:8579; PAPA2.
 DR H-InvDB; HIX0000282; -;
 DR MM; 602344; -;
 DR GO; GO:0005543; F:phospholipid binding; TAS.
 DR GO; GO:0006629; P:lipid metabolism; TAS.
 DR InterPro; IPR008262; Lipase AS.
 DR InterPro; IPR005065; PAF_ac_hydrolase II.
 DR InterPro; IPR000379; Ser_gstrs.
 DR Pfam; PF03403; PAF-AH_P_II; 1.
 DR PROSITE; PS0120; LIPASE_SER; 1.
 KW Direct protein sequencing; Hydrolase; Lipid degradation.
 FT ACT_SITE 236 236 Charge relay system (By similarity).
 FT ACT_SITE 259 259 Charge relay system (By similarity).
 FT ACT_SITE 314 314 Charge relay system (By similarity).
 FT CONFLICT 212 212 L -> F (in Ref. 2).
 SQ SEQUENCE 392 AA; 44035 MW; 690FB7E6F5B68317 CRC64;
 Query Match 33.8%; Score 797; DB 1; Length 392;
 Best Local Similarity 43.5%; Pred. No. 1.5e-53;
 Matches 163; Conservative 71; Mismatches 129; Indels 12; Gaps 6;
 QY 57 PRGNPGSVGCTDLMDHNTKGTFLRLYPYQDNDRL--DTLWIPNKEYFNGLSKFLGTH 114
 DB 10 PPTVTHLVGCGVMEQGNLQGSFRLFPYCPQKAEETMEQPLWIPRYEYCTGLAEYLPQN 69
 QY 115 WLMGNIL-RLFLGNTTPANNWNSPLRGEK-YPLVPSHGLGAFRTLYSAGIDLASHPG 172
 DB 70 KRCGGLLFNLAAGSCRLPVSWMNGPKTKDQSGYPLIIFSHGLGAFRTLYSAFCMELASRG 129
 QY 173 IVAAVEHRDRSASATYFK-----DQSAEIGDKSLVLRLLKQ-EEETHIRNEOVROA 226
 DB 130 VVAVPEHRDRSAAITYFCKQAPENQPTNESLQBEWIPFRVGEKEGFHVRNPQVORV 189
 QY 227 KECQALSLLIDHIGKPKVKNALDKFDMELQKSDIREKIAVIGSHSGGATVIOTLSED 286
 DB 190 SECLRVLKILQEVTAGQTVFNILPGGLDLMTLKGNDMSRVAVMGHSGFGATAILAKE 249
 QY 287 QRFCGIALDAMWPLGDVYSRIQPLFFINSEYFQVPANIIMKKCYSPDKERMTTI 346
 DB 250 TQFCRCAVALDAMWPLERDFYPKARGPVFFINTEKFQTMESVNLMMKKICAOHEQSRITV 309
 QY 347 RGSVHQNFADFTFATKLIQHML--KLKGDIDSNAIDLSNKASLAFLOKHLGLHKDFDQ 404
 DB 310 LGSVHRSGQTDFAFTVGNLIGKFFSTETRGSLDPYEGQGVWVRAMLAFLQKHLDLKEDYNQ 369
 QY 405 WDLIEGDDENLIPG 419
 DB 370 WNNLIEGIPSLTPG 384
 RESULT 14
 PAF2_BOVIN
 ID_PAF2_BOVIN STANDARD; PRT; 392 AA.
 AC P79106;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Platelet-activating factor acetylhydrolase 2, cytoplasmic
 DE (EC 3.1.1.47) (Serine dependent phospholipase A2).
 GN Name=PAFAH2;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

RC TISSUE=Kidney;
 RX MEDLINE=97115847; PubMed=8955149; DOI=10.1074/jbc.271.51.33032;
 RA Hattori K., Adachi H., Matsuzawa A., Yamamoto K., Tsujimoto M.,
 Aoki J., Hattori M., Arai H., Inoue K.;
 RT "CDNA cloning and expression of intracellular platelet-activating
 factor (PAF) acetylhydrolase II. Its homology with plasma PAF
 acetylhydrolase";
 RL J. Biol. Chem. 271:33032-33038(1996).
 RN [2]
 RP REVIEW.
 RX MEDLINE=97364701; PubMed=9218411; DOI=10.1074/jbc.272.29.17895;
 RA Stafforini D.M., McIntyre T.M., Zimmerman G.A., Prescott S.M.;
 RT "Platelet-activating factor acetylhydrolases";
 RL J. Biol. Chem. 272:17895-17898(1997).
 CC -!- FUNCTION: Has a marked selectivity for phospholipids with short
 acyl chains at the sn-2 position. May share a common physiologic
 function with the plasma-type enzyme.
 CC -!- CATALYTIC ACTIVITY: 1-alkyl-2-acetyl-sn-glycero-3-phosphocholine +
 H(2)O = 1-alkyl-sn-glycero-3-phosphocholine + acetate.
 CC -!- SUBUNIT: Monomer.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- TISSUE SPECIFICITY: Expressed at highest levels in liver and at
 lower levels in other tissues.
 CC -!- SIMILARITY: Belongs to the serine esterase family.
 CC -----
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
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 or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL; D87559; BAA13419.1; -;
 DR InterPro; IPR008262; Lipase AS.
 DR InterPro; IPR005065; PAF_Ac_hydrol_II.
 DR InterPro; IPR003379; Ser_Gestr.
 DR Pfam; PF03403; PAF-AH_P_II; 1.
 DR PROSITE; PS00120; LIPASE_SER; 1.
 DR Direct protein sequencing; Hydrolase; Lipid degradation.
 KW ACT_SITE 236 236 Charge relay system (By similarity).
 FT ACT_SITE 259 259 Charge relay system (By similarity).
 FT ACT_SITE 314 314 Charge relay system (By similarity).
 SQ SEQUENCE 392 AA; 43865 MW; 1DEACA2ADF4CEA8 CRC64;

 Query Match 31.7%; Score 747; DB 1; Length 392;
 Best Local Similarity 41.9%; Pred. No. 1.2e-49;
 Matches 157; Conservative 67; Mismatches 139; Indels 12; Gaps 6;

 QY 57 PRGNPYSVGTDLMFHTNKGTPRLRYPSQNDRL--DTLWTPNKEYFWGLSKFLGTH 114
 DB 10 PPVTGPHLVGCGDVMGQSLQSPFRLFPQCAEETSEQLWTPRYEYCAGLAEYLKFN 69

 QY 115 WLMGNIL-RLFLGSMWTPANNNSPLRGEK-YPLVVFHSGLGAFRTLYSAIGDILASHGF 172
 DB 70 KRWGGLNLFNGVSGCRPLVSMGPFKTKDGYPLIFSHGGAFTVYSAFCMELASRGF 129

 QY 173 IVAAVEHRDRSASATYFK-----DQSAEETGKSMYLRTRKQ-EBETHIRNEQVRQA 226
 DB 130 VVAVPEHRDGSAACTCKQTPENQPDNEALKEWIPHRQIEGEKEFVRYVYQVHQRV 189

 QY 227 KECQALSLILDIHGKVPKXNALDKFDMBOLKDSIDREKIAVIGHSGFGATVIQTLS 286
 DB 190 SECVRVLKIQEVTAGQAVLNILPGGLDMLTKGIDVSRVAVMGHSGFGATAILAKE 249

 QY 287 QRFCGIALDAWPEPLGDEVYSRIPQPLFFINSEYFOYPAIIMKKCYSPDKERKMITI 346
 DB 250 MQRFCAVALDAWPEPLSHDFYFTARGDFFIFNAEKFTQVETVNLMLKICDQHQSRIT 309

 QY 347 RGSVHQNFADFTATGKIIIGHMLK--LKGIDISNAADLSNKASLAPLQKHLGHKDFDQ 404
 DB 310 LGSVHRSLTDFVAVAGNWSKFFSSHTRGSLDPPVEGQETVVRVAVLAPLQKHLDKEDYDQ 369

QY 405 WDLIEGDDNENLIPG 419
 DB 370 WNNFIEGIGPSLTPG 384

 RESULT 15
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 ID Q6GPX8 PRELIMINARY; PRT; 362 AA.
 AC Q6GPX8;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE MGC82533 protein.
 GN Name=MGC82533;
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Splice;
 RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.2426038999;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
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 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
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 Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 Krzywinski M.I., Skalek U., Smalls D.E., Schnerch A., Schein J.E.,
 Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Splice;
 RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
 Richardson P.;
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
 initiative";
 RL Dev. Dyn. 225:384-391(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Splice;
 RA Klein S., Gerhard D.S.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC072977; AAH72977.1; -;
 DR GO; GO:0008247; C-2-acetyl-1-alkylglycerophosphocholine ester. ; IEA.
 DR GO; GO:0003847; F-1-alkyl-2-acetyl-1-alkylglycerophosphocholine ester. ; IEA.
 DR GO; GO:0003824; F-catalytic activity; IEA.
 DR GO; GO:0016042; P:lipid catabolism; IEA.
 DR InterPro; IPR008262; Lipase AS.
 DR InterPro; IPR005065; PAF_Ac_hydrol_II.
 DR InterPro; IPR003379; Ser_Gestr.
 DR Pfam; PF03403; PAF-AH_P_II; 1.
 DR PROSITE; PS00120; LIPASE_SER; UNKNOWN 1.
 SQ SEQUENCE 362 AA; 40280 MW; DAC93A288E9E837 CRC64;

 Query Match 29.5%; Score 696; DB 2; Length 362;
 Best Local Similarity 40.7%; Pred. No. 1e-45;
 Matches 146; Conservative 68; Mismatches 111; Indels 34; Gaps 7;


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Qy 71 MFDHTNKGTFURLYYP-SODNDRDLTLWI PNKEYFWGLSKELGTHW---LMGNILRLLPFG 126
Db 1 MVGHSKEGFFRLPYPCGSHDVQYPMWLPSEVVTALAKYLG--WDSSITPYISSLIFG 58

Qy 127 SMTTPANWNSPLRPG-EKYPLVVFVSHGLGAPRTLYSAIGIDLASHGFIVAAVEHRDRSAS 185
Db 59 HPQVPEVWSAPPVTVGVKKPLIIFSHGLGAPRTVVSALCMQLASHGFLVAALEHRDGSAC 118

Qy 186 ATYYFKDQ-----SAAEIGDKSWLYLRTLKQEEETHIRNEQVQPAKESQ 231
Db 119 ATYHFADDDPTNAPLKEVWVPFSKVEVGK-----BFLRNYQLHHRANECVR 166

Qy 232 ALSILIDIDHKGPKVKNALDLKFDMEQLKDSIDREKIAVIGHSGFGATVOTLSEDRFC 291
Db 167 VMQILRDINAG-VVFNVLKSDFDLQALKGRMDFNNVIMGHSFGASSTLLSLAKDDTFC 225

Qy 292 GIALDAMFPLGDEVYGRIPQPLFINSEYQYIPANIIMKKCYSPDKERMITIRGSVH 351
Db 226 AIALDAMFPLEDASYTNIQKPIILFINAEHFOTTSSIQKMKRLNAGNRESKAITILGSVH 285

Qy 352 QNFADPTFATGKIIGHMLKLGKGDIDSNAIDLKSLAFLOKHLGLHKDPQWDCLIE 410
Db 286 HSLSDSAFLSGFLADRILOPRAKLNPQCLOQTITSALSFLQKHLDPGNIPSLDLSLSE 344

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Search completed: March 15, 2005, 10:07:38
Job time : 167.294 secs

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OM protein - protein search, using sw model

Run on: March 15, 2005, 09:47:50 ; Search time 64.2647 Seconds
(without alignments)
1029.119 Million cell updates/sec

Title: US-09-922-067f-14_COPY_271_441

Perfect score: 912
Sequence: 1 GHSEFGATVITLSEDRFR.....INTNQHIMLQNSGIEKYN 171

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	912	100.0	441	3 AAB01942	Aab01942 Human low
2	912	100.0	441	5 AAE14750	Aae14750 Human lip
3	912	100.0	442	2 AAR64928	Aar64928 Human T-C
4	908	99.6	400	7 ADG73660	Adg73660 Human PAF
5	908	99.6	400	4 AAE00782	Aae00782 Mouse-Hum
6	908	99.6	440	4 AAE00783	Aae00783 Mouse-Hum
7	908	99.6	441	2 AAR71913	Aar71913 Human pla
8	908	99.6	441	2 AAR73046	Aar73046 Human ace
9	908	99.6	441	2 AAR73047	Aar73047 Human ace
10	908	99.6	441	2 AAR71920	Aar71920 Human ace
11	908	99.6	441	2 AAW23796	Aaw23796 Human pla
12	908	99.6	441	2 AA009808	Aa009808 Platelet-
13	908	99.6	441	2 AAW26498	Aaw26498 Human pla
14	908	99.6	441	2 AAW38361	Aaw38361 Human pla
15	908	99.6	441	2 AAW96334	Aaw96334 Human pla
16	908	99.6	441	2 AAW73359	Aaw73359 Human PAF
17	908	99.6	441	3 AAY88301	Aay88301 Human pla
18	908	99.6	441	3 AAY50735	Aay50735 Human PAF
19	908	99.6	441	3 AAB00774	Aab00774 Plasma pl
20	908	99.6	441	4 AAE00761	Aae00761 Human pla
21	908	99.6	441	4 AAE00777	Aae00777 Human pla
22	908	99.6	441	4 AAE00768	Aae00768 Human pla
23	908	99.6	441	4 AAE00778	Aae00778 Human pla
24	908	99.6	441	4 AAB49451	Aab49451 Platelet-
25	908	99.6	441	4 AAE15515	Aae15515 Human pla

26	908	99.6	441	4 AAE15524	Aae15524 Human pla
27	908	99.6	441	4 AAE15525	Aae15525 Human pla
28	908	99.6	441	4 AAE15507	Aae15507 Human pla
29	908	99.6	441	5 ABG61862	Abg61862 Prostate
30	908	99.6	441	6 ABP55072	Abp55072 Human lip
31	908	99.6	441	6 ADA19491	Ada19491 Human pla
32	908	99.6	441	7 ADP65141	Adp65141 Human pho
33	908	99.6	441	8 ADJ57408	Adj57408 Human pho
34	908	99.6	441	8 ADP12938	Adp12938 Protein e
35	908	99.6	441	8 ADR14277	Adr14277 Human NF-
36	908	99.6	441	8 ADR51543	Adr51543 Human lip
37	908	99.6	441	8 ADP54611	Adp54611 Human PRO
38	908	99.6	441	8 ADP23967	Adp23967 PRO polyyp
39	908	99.6	520	7 ADG73668	Adg73668 Human HCB
40	908	99.6	638	7 ADG73670	Adg73670 Human GCB
41	908	99.6	642	7 ADG73672	Adg73672 Human aCB
42	905	99.2	441	2 AAR71921	Aar71921 Human ace
43	905	99.2	441	4 AAE00769	Aae00769 Human pla
44	905	99.2	441	4 AAE15516	Aae15516 Human pla
45	903	99.0	441	4 AAE00771	Aae00771 Human pla

ALIGNMENTS

RESULT 1
AAB01942
ID AAB01942 standard; protein; 441 AA.
XX AC AAB01942;
XX DT 18-SEP-2000 (first entry)
XX DE Human low density lipoprotein-associated phospholipase A2 (LDL-PLA2).
XX KW Human; low density lipoprotein associated phospholipase A2; LDL-PLA2;
XX KW plasma PAF acetyl hydroxylase; recombinant; purification;
XX KW short chain phospholipid; serine-dependent phospholipase; inflammation;
XX KW proinflammatory; anti inflammatory; drug screening; antibody; diagnosis.
XX OS Homo sapiens.
XX FN WO200024910-A1.
XX PD 04-MAY-2000.
XX PF 27-OCT-1999; 99WO-GB003551.
XX PR 28-OCT-1998; 98GB-00023647.
XX PR 28-OCT-1998; 98GB-00023648.
XX PA (SMIK) SMITHKLINE BEECHAM PLC.
XX FI Boyd H, Tew DG;
XX DR WPI; 2000-350749/30.
XX DR N-PSDB; AAA52357.
XX PT Recombinant low density lipoprotein associated phospholipase A2, used to
XX PT produce antibodies for diagnostics, is purified using a Blue Sepharose
XX PS and Q Sepharose column.
XX PS Claim 6b; Page 17; 28pp; English.
XX CC The present sequence represents human LDL-PLA2. The invention relates to
XX CC a method for purifying recombinant low density lipoprotein-associated
XX CC phospholipase A2 (LDL-PLA2). The method comprises applying a cell
XX CC extract, supernatant or solution containing the recombinantly expressed
XX CC LDL-PLA2 to a zinc chelating column, applying the eluate to a Blue
XX CC Sepharose column, and applying that eluate to a Q Sepharose column. The
XX CC invention also provides a process which additionally comprises the prior
XX CC steps of constructing a vector comprising a cDNA encoding a histidine
XX CC tagged LDL-PLA2 or fragment thereof, expressing the tagged protein in a

CC host cell, isolating the tagged protein from the harvest medium or cell
 CC lysate, purifying the protein using a metal matrix affinity column
 CC (preferably a nickel column), and removing the histidine tag by protease
 CC cleavage. LDL-PLA2, also known as plasma PAF acetyl hydroxylase, is a
 CC serine-dependent phospholipase which catalyses the hydrolysis of
 CC phospholipids with short chain acyl groups at the sn-2 position. Its in
 CC vivo role is not known - due to its ability to hydrolyse both
 CC phospholipids with short chain sn-2 substituents (which often arise from
 CC oxidative cleavage of longer chain sn-2 substituents) and PAF, it may be
 CC either a pro-inflammatory enzyme or an anti-inflammatory enzyme,
 CC depending on the precise in vivo role adopted. LDL-PLA2 can be used in
 CC structural and mechanistic studies to elucidate the activity of the
 CC enzyme in vivo. The enzyme may be used to screen and identify compounds
 CC which modulate its activity, and to raise antibodies for use in
 CC diagnostics
 CC
 XX
 SQ Sequence 441 AA;

Query Match 100.0%; Score 912; DB 3; Length 441;
 Best Local Similarity 100.0%; Pred. No. 2.5e-98;
 Matches 171; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHSFGGATVIQTLSSEDRFCGIALDAWMPPLGDEVYSRIPOPLFFINSYFOYPANIIK 60
 |||||
 DB 271 GHSFGGATVIQTLSSEDRFCGIALDAWMPPLGDEVYSRIPOPLFFINSYFOYPANIIK 330
 |||||

QY 61 MKKCYSPDKERKMITIRGSHQNFADFTFATGKIIGHMLKLGKIDSNAAIDLSNKA 120
 |||||
 DB 331 MKKCYSPDKERKMITIRGSHQNFADFTFATGKIIGHMLKLGKIDSNAAIDLSNKA 390
 |||||

QY 121 FLQKHLGLHKDFQWDCLEGGDENLPGTNTNTNQHIMLQNSSGIEKYN 171
 |||||
 DB 391 FLQKHLGLHKDFQWDCLEGGDENLPGTNTNTNQHIMLQNSSGIEKYN 441
 |||||

RESULT 2
 AAE14750
 ID AAE14750 standard; protein; 441 AA.
 AC AAE14750;
 XX
 DT 04-OCT-2002 (first entry)
 XX
 DE Human lipoprotein-associated phospholipase A2.
 XX
 KW Atherosclerosis; single nucleotide polymorphism; SNP;
 KW lipoprotein-associated phospholipase A2; Lp-PLA2; human.
 XX
 OS Homo sapiens.
 XX
 PN WO200236817-A2.
 XX
 PD 10-MAY-2002.
 XX
 PF 02-NOV-2001; 2001WO-GB004876.
 XX
 PR 04-NOV-2000; 2000GB-00027181.
 XX
 XX (SMIK) SMITHKLINE BEECHAM PLC.
 XX
 XX Campbell D, Meginnins R, Spurr N, Valdes AM;
 XX
 XX WPI; 2002-479764/51.
 DR N-PSDB; AAD36733.
 XX
 XX Diagnosing atherosclerosis or predicting susceptibility of a subject to
 PT atherosclerosis by determining single nucleotide polymorphism in Lp-PLA2-
 PT encoding polynucleotide.
 XX
 XX Disclosure; Page 14; 30pp; English.
 PS
 XX The invention relates to a method of diagnosing atherosclerosis or
 XX predicting the susceptibility of a subject to atherosclerosis, comprising

CC determining the presence or absence of a single nucleotide polymorphism
 CC (SNP) in codon 379 of a lipoprotein-associated phospholipase A2 (Lp-PLA2)
 CC -encoding polynucleotide, where the codon comprising the SNP encodes an
 CC amino acid other than valine. The method is useful for predicting the
 CC likelihood of developing atherosclerosis, predicting and responding to
 CC the progression of the atherosclerotic condition and drug treatment, or
 CC predicting disease outcome in a subject. The method is also useful in the
 CC selection of patient groups for conducting clinical trials concerning
 CC therapeutic compounds with potential for use in the treatment of
 CC atherosclerosis. The present sequence is human lipoprotein-associated
 CC phospholipase A2
 CC
 XX
 SQ Sequence 441 AA;

Query Match 100.0%; Score 912; DB 5; Length 441;
 Best Local Similarity 100.0%; Pred. No. 2.5e-98;
 Matches 171; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GHSFGGATVIQTLSSEDRFCGIALDAWMPPLGDEVYSRIPOPLFFINSYFOYPANIIK 60
 |||||
 DB 271 GHSFGGATVIQTLSSEDRFCGIALDAWMPPLGDEVYSRIPOPLFFINSYFOYPANIIK 330
 |||||

QY 61 MKKCYSPDKERKMITIRGSHQNFADFTFATGKIIGHMLKLGKIDSNAAIDLSNKA 120
 |||||
 DB 331 MKKCYSPDKERKMITIRGSHQNFADFTFATGKIIGHMLKLGKIDSNAAIDLSNKA 390
 |||||

QY 121 FLQKHLGLHKDFQWDCLEGGDENLPGTNTNTNQHIMLQNSSGIEKYN 171
 |||||
 DB 391 FLQKHLGLHKDFQWDCLEGGDENLPGTNTNTNQHIMLQNSSGIEKYN 441
 |||||

RESULT 3
 AAR64928
 ID AAR64928 standard; protein; 442 AA.
 AC AAR64928;
 XX
 DT 25-MAR-2003 (revised)
 DT 18-AUG-1995 (first entry)
 XX
 DE Human T-cell lymphoma lipoprotein-associated phospholipase-A2.
 XX
 KW T-cell; T-lymphocyte; lipoprotein-associated phospholipase-A2; enzyme;
 KW atherosclerosis; diagnosis; therapy; antiarteriosclerotic.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 25..31
 FT /note= "Peptide 4"
 FT 115..133
 FT /note= "Peptide 3"
 FT 298..327
 FT /note= "Peptide 2"
 FT 368..393
 FT /note= "Peptide 1"
 XX
 PN WO9500649-A1.
 XX
 PD 05-JAN-1995.
 XX
 PF 24-JUN-1994; 94WO-GB001374.
 XX
 PR 25-JUN-1993; 93GB-00013144.
 PR 11-JAN-1994; 94GB-00000413.
 XX
 XX (SMIK) SMITHKLINE BEECHAM PLC.
 XX
 XX Macphree CH, Tew DG, Southan CD, Hickey DMB, Gloger IS;
 PI Lawrence GMP, Rice SQJ;
 XX WPI; 1995-052086/07.
 DR N-PSDB; AAQ81780.

XX Purified lipoprotein associated phospholipase A2 - used to develop prods.
PT for diagnosis and therapy, partic. inhibitors for treatment of
PT atherosclerosis.
XX
XX Claim 8; Page 19; 29pp; English.
XX
XX This sequence encodes an enzyme which may be used in a method of
CC screening compounds to identify those compounds which inhibit Lp-PLA2
CC which involves contacting isolated Lp-PLA2 with a test compound and
CC measuring the rate of turnover of an enzyme substrate as compared with
CC the rate of turnover in the absence of the test compound. (Updated on 25-
CC MAR-2003 to correct PN field.)
XX
XX Sequence 442 AA;
SQ
Query Match 100.0%; Score 912; DB 2; Length 442;
Best Local Similarity 100.0%; Pred. No. 2.5e-98;
Matches 171; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GHSFGGATVIQTLSQDQFRFCGIALDAWMPPLGDEVYSRIPQPLFFINSEYFQYVPAIIK 60
DB 271 GHSFGGATVIQTLSQDQFRFCGIALDAWMPPLGDEVYSRIPQPLFFINSEYFQYVPAIIK 330
QY 61 MKKCYSPDKERKMITIRGSHVQNFADTFATGKIIGHMLKLGKIDSNAAIDLSNKASLA 120
DB 331 MKKCYSPDKERKMITIRGSHVQNFADTFATGKIIGHMLKLGKIDSNAAIDLSNKASLA 390
QY 121 FLQKHLGLHKDFQDCLIEGDDENLIPGNTINTNQHIMLQNSSGIEKYN 171
DB 391 FLQKHLGLHKDFQDCLIEGDDENLIPGNTINTNQHIMLQNSSGIEKYN 441
RESULT 4
ADG73660
ID ADG73660 standard; protein; 400 AA.
XX
AC ADG73660;
XX
XX 11-MAR-2004 (first entry)
XX Human PAF-AH SEQ ID NO:8.
XX collagenase; collagen; platelet activating factor; acetyl hydrolase;
XX collagen coupling region; antiinflammatory; inflammation;
XX skin transplantation; human.
XX Homo sapiens.
XX JP2003284553-A.
XX
XX 07-OCT-2003.
XX
XX 28-MAR-2002; 2002JP-00090847.
XX
XX 28-MAR-2002; 2002JP-00090847.
XX (SEKG) SEIKAGAKU KOGYO CO LTD.
XX
XX WPI; 2003-869686/81.
XX N-PSDB; ADG73659.
XX
XX Novel bioactive protein binding with collagen and having platelet
PT activating factor and acetyl hydrolase activity, useful for suppressing
PT local inflammation.
XX
XX Claim 2; SEQ ID NO 8; 53pp; Japanese.
XX
XX The invention relates to a novel bioactive protein binding with collagen
CC having platelet activating factor and acetyl hydrolase activity, and
CC comprising collagen coupling region. A protein of the invention has
CC antiinflammatory activity. A protein of the invention is useful for
CC suppressing local inflammation caused during skin transplantation. The

CC present sequence is used in the exemplification of the invention.
XX
SQ Sequence 400 AA;
Query Match 99.6%; Score 908; DB 7; Length 400;
Best Local Similarity 99.4%; Pred. No. 6.4e-98;
Matches 170; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GHSFGGATVIQTLSQDQFRFCGIALDAWMPPLGDEVYSRIPQPLFFINSEYFQYVPAIIK 60
DB 230 GHSFGGATVIQTLSQDQFRFCGIALDAWMPPLGDEVYSRIPQPLFFINSEYFQYVPAIIK 289
QY 61 MKKCYSPDKERKMITIRGSHVQNFADTFATGKIIGHMLKLGKIDSNAAIDLSNKASLA 120
DB 290 MKKCYSPDKERKMITIRGSHVQNFADTFATGKIIGHMLKLGKIDSNAAIDLSNKASLA 349
QY 121 FLQKHLGLHKDFQDCLIEGDDENLIPGNTINTNQHIMLQNSSGIEKYN 171
DB 350 FLQKHLGLHKDFQDCLIEGDDENLIPGNTINTNQHIMLQNSSGIEKYN 400
RESULT 5
AAE00782
ID AAE00782 standard; protein; 440 AA.
XX
AC AAE00782;
XX
DT 11-SEP-2003 (revised)
DT 02-JUL-2001 (first entry)
XX
DE Mouse-Human plasma PAF-AH fusion protein from plasmid pRC/pH.MHC1.
XX
XX Human; platelet-activating factor acetylhydrolase; PAF-AH; arthritis;
XX antiinflammatory; septicaemia; inflammation; haemostasis; parturition;
XX asthma; anaphylaxis; septic shock; antibacterial; fusion protein.
XX
XX Mus sp.
XX Homo sapiens.
XX Chimeric.
XX
XX Key Location/Qualifiers
XX Region 1..97
XX /note= "Corresponds to N-terminal 97 amino acids of mouse
XX plasma platelet-activating factor acetylhydrolase (PAF-
XX AH)"
XX Region 98..440
XX /note= "Corresponds to C-terminal 343 amino acids of
XX human plasma platelet-activating factor acetylhydrolase
XX (PAF-AH)"
XX
XX US6203790-B1.
XX
XX 20-MAR-2001.
XX
XX 23-MAY-2000; 2000US-00577758.
XX
XX 06-OCT-1993; 93US-00133803.
XX 06-OCT-1994; 94US-00318905.
XX 07-JUN-1995; 95US-00480658.
XX 22-JAN-1998; 98US-00010715.
XX
XX (ICOS-) ICOS CORP.
XX
XX Cousins LS, Eberhardt CD, Gray P, Trong HL, Tjoelker LW;
XX Wilder CU;
XX
XX WPI; 2001-280610/29.
XX N-PSDB; AAD04168.
XX
XX Treating a mammal susceptible to or suffering from septicemia comprises
PT administering a platelet-activating factor acetyl hydrolase (PAF-AH) to
PT supplement endogenous PAF-AH activity and to inactivate pathological
PT amounts of PAF.

XX Example 8; Col; 54pp; English.

PS The present sequence is mouse-human plasma platelet-activating factor

XX acetylhydrolase (PAF-AH) fusion protein construct from plasmid

CC pRc/PH.MHC1. The invention relates to human plasma platelet-activating

CC factor acetylhydrolase (PAF-AH) and its corresponding cDNA molecule. The

CC invention also relates to method of treating a mammal susceptible to or

CC suffering from septicemia. PAF functions in normal physiological

CC processes such as inflammation, haemostasis and parturition. PAF-AH

CC specific antibodies are used in the diagnostic methods to detect abnormal

CC levels of PAF-AH in serum and also for treating the pathological

CC inflammatory conditions of PAF-AH such as asthma, anaphylaxis, septic

CC shock and arthritis. PAF-AH antibody is also useful for screening a

CC genetic lesion in the human plasma PAF-AH gene, which occurs due to the

CC replacement of nucleotide G to T at position 996 within exon 9 resulting

CC in replacement of amino acid Val to Phe at position 279. Thus the

CC deficiency of PAF-AH activity is due to the genetic lesion in human

CC plasma PAF-AH gene. (Updated on 11-SEP-2003 to standardise OS field)

XX

SQ Sequence 440 AA;

Query Match 99.6%; Score 908; DB 4; Length 440;

Best Local Similarity 99.4%; Pred. No. 7.4e-98;

Matches 170; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHSFGGATVIQTLSEDRFCRGIALDAWMPPLGDEVYSRIPQLFFINSEYFOYPANIIK 60

DB 270 GHSFGGATVIQTLSEDRFCRGIALDAWMPPLGDEVYSRIPQLFFINSEYFOYPANIIK 329

QY 61 MKKCYSPDKERKMITIRGSHVQNFADFTATGKIIGHMLKLGKIDSDNAIDLSNKASLA 120

DB 330 MKKCYSPDKERKMITIRGSHVQNFADFTATGKIIGHMLKLGKIDSDNVAIDLSNKASLA 389

QY 121 FLQKHLGLHKDFDQWDCLEGGDENLPGTNTNTNQHIMLQNSSGIEKYN 171

DB 390 FLQKHLGLHKDFDQWDCLEGGDENLPGTNTNTNQHIMLQNSSGIEKYN 440

RESULT 6

AAE00783

ID AAE00783 standard; protein; 440 AA.

XX

AC AAE00783;

XX

DT 11-SEP-2003 (revised)

DT 02-JUL-2001 (first entry)

DE Mouse-Human plasma PAF-AH fusion protein from plasmid pRc/PH.MHC2.

XX

KW Human; platelet-activating factor acetylhydrolase; PAF-AH; arthritis;

KW antiinflammatory; septicemia; inflammation; haemostasis; parturition;

KW asthma; anaphylaxis; septic shock; antibacterial; fusion protein.

XX

OS Mus sp.

OS Homo sapiens.

OS Chimeric.

XX

PH Key Location/Qualifiers

FT 1..40

FT /note= "Corresponds to N-terminal 40 amino acids of mouse

FT plasma platelet-activating factor acetylhydrolase (PAF-

FT AH)"

FT

FT Region 41..440

FT /note= "Corresponds to C-terminal 400 amino acids of

FT human plasma platelet-activating factor acetylhydrolase

FT (PAF-AH)"

XX

XX US6203790-B1.

XX

XX 20-MAR-2001.

XX

XX 23-MAY-2000; 2000US-00577758.

XX

PR 06-OCT-1993; 93US-00133803.

PR 06-OCT-1994; 94US-00318905.

PR 07-JUN-1995; 95US-00480658.

PR 22-JAN-1998; 98US-00010715.

XX (ICOS-) ICOS CORP.

PA Cousins LS, Eberhardt CD, Gray P, Trong HL, Tjoelker LW;

PI Wilder CL;

XX

XX WPI; 2001-280610/29.

DR N-PSDB; AAD04169.

XX

XX Treating a mammal susceptible to or suffering from septicemia comprises

PT administering a platelet-activating factor acetyl hydrolase (PAF-AH) to

PT supplement endogenous PAF-AH activity and to inactivate pathological

PT amounts of PAF.

XX

PS Example 8; Col; 54pp; English.

XX

CC The present sequence is mouse-human plasma platelet-activating factor

CC acetylhydrolase (PAF-AH) fusion protein construct from plasmid

CC pRc/PH.MHC2. The invention relates to human plasma platelet-activating

CC factor acetylhydrolase (PAF-AH) and its corresponding cDNA molecule. The

CC invention also relates to method of treating a mammal susceptible to or

CC suffering from septicemia. PAF functions in normal physiological

CC processes such as inflammation, haemostasis and parturition. PAF-AH

CC specific antibodies are used in the diagnostic methods to detect abnormal

CC levels of PAF-AH in serum and also for treating the pathological

CC inflammatory conditions of PAF-AH such as asthma, anaphylaxis, septic

CC shock and arthritis. PAF-AH antibody is also useful for screening a

CC genetic lesion in the human plasma PAF-AH gene, which occurs due to the

CC replacement of nucleotide G to T at position 996 within exon 9 resulting

CC in replacement of amino acid Val to Phe at position 279. Thus the

CC deficiency of PAF-AH activity is due to the genetic lesion in human

CC plasma PAF-AH gene. (Updated on 11-SEP-2003 to standardise OS field)

XX

SQ Sequence 440 AA;

Query Match 99.6%; Score 908; DB 4; Length 440;

Best Local Similarity 99.4%; Pred. No. 7.4e-98;

Matches 170; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHSFGGATVIQTLSEDRFCRGIALDAWMPPLGDEVYSRIPQLFFINSEYFOYPANIIK 60

DB 270 GHSFGGATVIQTLSEDRFCRGIALDAWMPPLGDEVYSRIPQLFFINSEYFOYPANIIK 329

QY 61 MKKCYSPDKERKMITIRGSHVQNFADFTATGKIIGHMLKLGKIDSDNAIDLSNKASLA 120

DB 330 MKKCYSPDKERKMITIRGSHVQNFADFTATGKIIGHMLKLGKIDSDNVAIDLSNKASLA 389

QY 121 FLQKHLGLHKDFDQWDCLEGGDENLPGTNTNTNQHIMLQNSSGIEKYN 171

DB 390 FLQKHLGLHKDFDQWDCLEGGDENLPGTNTNTNQHIMLQNSSGIEKYN 440

RESULT 7

AAE071913

ID AAE071913 standard; protein; 441 AA.

XX

AC AAE071913;

XX

DT 25-MAR-2003 (revised)

DT 05-DEC-1995 (first entry)

XX

XX Human plasma platelet activating factor, acetyl hydrolase (PAF-AH).

XX Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;

XX disease; pleurisy; diagnosis.

XX

OS Homo sapiens.

```
PN W09509921-A1.
XX
PD 13-APR-1995.
XX
XX 06-OCT-1994; 94WO-US011340.
XX
XX 06-OCT-1993; 93US-00133803.
XX
XX (ICOS-) ICOS CORP.
XX
XX Cousins LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;
PI Wilder CL;
XX
XX WPI; 1995-155262/20.
XX
XX New nucleic acid encoding platelet activating factor, acetyl:hydrolase -
XX useful in diagnosis and for treating inflammatory diseases, e.g.
XX
XX Example 10; Page 54; 89pp; English.
XX
XX The human acetyl hydrolase gene (AAQ87947) has been isolated and
XX purified. The platelet activating factor acetyl hydrolase (AAR71913) is
XX useful in the treatment of inflammatory diseases, in particular pleurisy,
XX asthma, rhinitis and eczema. The gene may also be used in raising
XX monoclonal antibodies specific for PAF-AH that are useful in the
XX diagnosis of such diseases. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 441 AA;
SQ
Query Match 99.6%; Score 908; DB 2; Length 441;
Best Local Similarity 99.4%; Pred. No. 7.4e-98;
Matches 170; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GHSFGGATVQTLSERQRCGIALDAWMPPLGDEVYSRIPQPLFFINSEYFOYPANIIK 60
DB 271 GHSFGGATVQTLSERQRCGIALDAWMPPLGDEVYSRIPQPLFFINSEYFOYPANIIK 330
QY 61 MKKCYSPDKERKMITIRGSHQNFADFTFATGKIIGHMLKLGKIDNSNAIDLNSKASLA 120
DB 331 MKKCYSPDKERKMITIRGSHQNFADFTFATGKIIGHMLKLGKIDNSNAIDLNSKASLA 390
QY 121 FLQHLGLHKDFDQWDCLEGGDENLIPGTNTNTNOHIMLQNSSGIEKYN 171
DB 391 FLQHLGLHKDFDQWDCLEGGDENLIPGTNTNTNOHIMLQNSSGIEKYN 441
RESULT 8
AAR73046
ID AAR73046 standard; protein; 441 AA.
XX
XX AAR73046;
XX
XX 25-MAR-2003 (revised)
DT 06-DEC-1995 (first entry)
XX
XX Human acetyl hydrolase (AH) mutant C67S.
XX
XX Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;
XX disease; pleurisy; diagnosis.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Misc-difference 67 /note= "Wild-type Cys is substd. by Ser."
XX
XX W09509921-A1.
XX
XX 13-APR-1995.
XX
XX 06-OCT-1994; 94WO-US011340.
XX
XX 06-OCT-1993; 93US-00133803.
XX
XX (ICOS-) ICOS CORP.
XX
XX Cousins LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;
PI Wilder CL;
XX
XX WPI; 1995-155262/20.
XX
XX New nucleic acid encoding platelet activating factor, acetyl:hydrolase -
XX useful in diagnosis and for treating inflammatory diseases, e.g.
XX
XX Example 5; Page 53-54; 89pp; English.
XX
XX The human acetyl hydrolase gene (AAQ87947) has been isolated and
XX purified. The platelet activating factor acetyl hydrolase (AAR71913) is
XX useful in the treatment of inflammatory diseases, in particular pleurisy,
XX asthma, rhinitis and eczema. The gene may also be used in raising
XX monoclonal antibodies specific for PAF-AH that are useful in the
XX diagnosis of such diseases. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 441 AA;
SQ
Query Match 99.6%; Score 908; DB 2; Length 441;
Best Local Similarity 99.4%; Pred. No. 7.4e-98;
Matches 170; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GHSFGGATVQTLSERQRCGIALDAWMPPLGDEVYSRIPQPLFFINSEYFOYPANIIK 60
DB 271 GHSFGGATVQTLSERQRCGIALDAWMPPLGDEVYSRIPQPLFFINSEYFOYPANIIK 330
QY 61 MKKCYSPDKERKMITIRGSHQNFADFTFATGKIIGHMLKLGKIDNSNAIDLNSKASLA 120
DB 331 MKKCYSPDKERKMITIRGSHQNFADFTFATGKIIGHMLKLGKIDNSNAIDLNSKASLA 390
QY 121 FLQHLGLHKDFDQWDCLEGGDENLIPGTNTNTNOHIMLQNSSGIEKYN 171
DB 391 FLQHLGLHKDFDQWDCLEGGDENLIPGTNTNTNOHIMLQNSSGIEKYN 441
RESULT 9
AAR73047
ID AAR73047 standard; protein; 441 AA.
XX
XX AAR73047;
XX
XX 25-MAR-2003 (revised)
DT 06-DEC-1995 (first entry)
XX
XX Human acetyl hydrolase (AH) mutant C229S.
XX
XX Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;
XX disease; pleurisy; diagnosis.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Misc-difference 229 /note= "Wild-type Cys is substd. by Ser."
XX
XX W09509921-A1.
XX
XX 13-APR-1995.
XX
XX 06-OCT-1994; 94WO-US011340.
XX
XX 06-OCT-1993; 93US-00133803.
XX
XX
```

XX (ICOS-) ICOS CORP.
 XX Cousins LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;
 XX Wilder CL;
 XX WPI; 1995-155262/20.
 XX New nucleic acid encoding platelet activating factor, acetyl:hydrolase -
 XX useful in diagnosis and for treating inflammatory diseases, e.g.
 XX pleurisy.
 XX Example 10; Page ?; 89pp; English.
 XX The human acetyl hydrolase (AH) gene (AAQ87947) has been isolated and
 XX purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were
 XX made with single amino acid changes for the purposes of identifying the
 XX active site of AH. The sequences of these mutants are not given in the
 XX patent specification; they have been derived from the original wild-type
 XX protein (AAR71913). The AH gene and its product are useful in the
 XX treatment of inflammatory diseases, in particular pleurisy, asthma,
 XX rhinitis and eczema. The gene may also be used in raising monoclonal
 XX antibodies specific for AH that are useful in the diagnosis of such
 XX diseases. (Updated on 25-MAR-2003 to correct PN field.)
 XX Sequence 441 AA;
 SQ Query Match 99.6%; Score 908; DB 2; Length 441;
 Best Local Similarity 99.4%; Pred. No. 7.4e-98;
 Matches 170; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GHSFGGATVIQTISEDQRCGIALDAWMPPLGDEVYSRIPQPLFFINSEYFOYPAIIK 60
 DB 271 GHSFGGATVIQTISEDQRCGIALDAWMPPLGDEVYSRIPQPLFFINSEYFOYPAIIK 330
 QY 61 MKKCYSPDKERKMITIRGSHQNFADFTFATGKIIGHMLKLGKIDNSNAIDLSNKASLA 120
 DB 331 MKKCYSPDKERKMITIRGSHQNFADFTFATGKIIGHMLKLGKIDNSNAIDLSNKASLA 390
 QY 121 FLQKHGLHKDFQWDCLIEGDENLIPGTNINTNQHIMLQNSSGIEKYN 171
 DB 391 FLQKHGLHKDFQWDCLIEGDENLIPGTNINTNQHIMLQNSSGIEKYN 441
 RESULT 10
 AAR71920
 ID AAR71920 standard; protein; 441 AA.
 XX AC AAR71920;
 XX DT 25-MAR-2003 (revised)
 XX DT 06-DEC-1995 (first entry)
 XX DE Human acetyl hydrolase (AH) mutant S108A.
 XX KW Acetyl hydrolase; AH; platelet activating factor; PAF; inflammatory;
 XX KW disease; pleurisy; diagnosis.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 XX FT Misc-difference 108
 XX FT /note= "Wild-type Ser is substd. by Ala."
 XX WO9509921-A1.
 XX PN 13-APR-1995.
 XX PD 06-OCT-1994; 94WO-US011340.
 XX PF 06-OCT-1993; 93US-00133803.
 XX PR (ICOS-) ICOS CORP.
 XX PA Tjoelker LW, Trong HL, Cousins LS, Wilder CL, Eberhardt CD;

XX Cousins LS, Eberhardt CD, Gray P, Le Trong H, Tjoelker LW;
 XX Wilder CL;
 XX WPI; 1995-155262/20.
 XX New nucleic acid encoding platelet activating factor, acetyl:hydrolase -
 XX useful in diagnosis and for treating inflammatory diseases, e.g.
 XX pleurisy.
 XX Example 10; Page ?; 88pp; English.
 XX The human acetyl hydrolase (AH) gene (AAQ87947) has been isolated and
 XX purified. Several mutant clones of AH (AAR71920-25 and AAR73046-49) were
 XX made with single amino acid changes for the purposes of identifying the
 XX active site of AH. The sequences of these mutants are not given in the
 XX patent specification; they have been derived from the original wild-type
 XX protein (AAR71913). The AH gene and its product are useful in the
 XX treatment of inflammatory diseases, in particular pleurisy, asthma,
 XX rhinitis and eczema. The gene may also be used in raising monoclonal
 XX antibodies specific for AH that are useful in the diagnosis of such
 XX diseases. (Updated on 25-MAR-2003 to correct PN field.)
 XX Sequence 441 AA;
 SQ Query Match 99.6%; Score 908; DB 2; Length 441;
 Best Local Similarity 99.4%; Pred. No. 7.4e-98;
 Matches 170; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GHSFGGATVIQTISEDQRCGIALDAWMPPLGDEVYSRIPQPLFFINSEYFOYPAIIK 60
 DB 271 GHSFGGATVIQTISEDQRCGIALDAWMPPLGDEVYSRIPQPLFFINSEYFOYPAIIK 330
 QY 61 MKKCYSPDKERKMITIRGSHQNFADFTFATGKIIGHMLKLGKIDNSNAIDLSNKASLA 120
 DB 331 MKKCYSPDKERKMITIRGSHQNFADFTFATGKIIGHMLKLGKIDNSNAIDLSNKASLA 390
 QY 121 FLQKHGLHKDFQWDCLIEGDENLIPGTNINTNQHIMLQNSSGIEKYN 171
 DB 391 FLQKHGLHKDFQWDCLIEGDENLIPGTNINTNQHIMLQNSSGIEKYN 441
 RESULT 11
 AAW23796
 ID AAW23796 standard; protein; 441 AA.
 XX AC AAW23796;
 XX DT 25-MAR-2003 (revised)
 XX DT 04-NOV-1997 (first entry)
 XX DE Human plasma platelet activating factor acetylhydrolase.
 XX KW Human PAF-AH; asthma; anaphylaxis; shock; anti-inflammatory;
 XX KW pro-inflammatory arachidonic acid metabolite; reperfusion injury;
 XX KW central nervous system shock; arthritis; Crohn's disease;
 XX KW systemic lupus erythematosus; adult respiratory distress syndrome.
 XX OS Homo sapiens.
 XX PN US5641669-A.
 XX PD 24-JUN-1997.
 XX PF 06-OCT-1994; 94US-00318905.
 XX PR 06-OCT-1993; 93US-00133803.
 XX PA (ICOS-) ICOS CORP.
 XX Tjoelker LW, Trong HL, Cousins LS, Wilder CL, Eberhardt CD;
 XX Gray P;

DR WPI; 1997-340947/31.
XX N-PSDB; AAT80564.
PT New human plasma platelet activating factor acetylhydrolase - useful as
PT anti-inflammatory for treatment of asthma, anaphylaxis, shock, etc.
XX
PS Claim 1; Col 35-38; 43pp; English.
XX
CC The present sequence represents the purified and isolated human plasma
CC platelet activating factor acetylhydrolase (PAF-AH). This novel
CC polypeptide inactivates PAF and oxidatively fragmented phospholipids such
CC as pro-inflammatory arachidonic acid metabolites, and so can be used to
CC treat inflammation by augmenting endogenous activity. Typical
CC applications are in asthma, anaphylaxis, shock, reperfusion injury, lupus
CC central nervous system shock, arthritis, Crohn's disease, systemic
CC erythematous, adult respiratory distress syndrome. The polypeptide can
CC also be used to raise specific antibodies (Ab) which are useful as
CC immunocassay reagents and for generating anti-idiotypic antibodies. The
CC nucleic acid encoding the protein can be used to screen for related genes
CC ; in hybridisation assays to assess the protein- producing cells; to
CC generate knockout mice; to detect genetic mutations and (antisense
CC sequences) to inhibit the protein expression. Unlike PAF receptor
CC antagonists, the protein is a natural component of plasma. (Updated on 25
CC -MAR-2003 to correct PF field.)
XX
SQ Sequence 441 AA;

Query Match 99.6%; Score 908; DB 2; Length 441;
Best Local Similarity 99.4%; Pred. No. 7.4e-98;
Matches 170; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHSPGGATVIQTISEDQRFRCGIALDAWMPPLGDEVYSRIPOPLFFINSEYFOYPANIIK 60
DB 271 GHSPGGATVIQTISEDQRFRCGIALDAWMPPLGDEVYSRIPOPLFFINSEYFOYPANIIK 330
QY 61 MKKCYSPDKERKMTITIGSVHQNFADEFTATGKIIGHMLKLGKIDSNVAIDLNSKASLA 120
DB 331 MKKCYSPDKERKMTITIGSVHQNFADEFTATGKIIGHMLKLGKIDSNVAIDLNSKASLA 390
QY 121 FLQKHLGLHKDFQDQWDCLEGGDENLIPGNTNTNOHIMLQNSSGIEKYN 171
DB 391 FLQKHLGLHKDFQDQWDCLEGGDENLIPGNTNTNOHIMLQNSSGIEKYN 441

RESULT 12
AAW09808
ID AAW09808 standard; protein; 441 AA.
AC AAW09808;
XX
XX 25-MAR-2003 (revised)
DT 12-JUN-1997 (first entry)
XX
XX Platelet-activating factor acetylhydrolase.
DE
XX Human platelet-activating factor acetylhydrolase; PAF-AH; detection;
KW mutation; V279F; substitution; restriction fragment length polymorphism;
KW analysis; diagnosis; inherited; deficiency; severe respiratory symptom;
KW asthmatic children; treat; inflammatory condition.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH 1. 41
FT /label= signal peptide
FT /note= "possibly contains additional peptide that is
FT cleaved to yield the mature functional enzyme"
FT Protein 42. .441
FT /label= mature_enzyme
FT Active-site 271. .275
FT /note= "contains active site serine; conforms to
FT consensus motif for mammalian and microbial lipases and
FT serine proteases"

XX US5605801-A.
XX 25-FEB-1997.
XX
XX 07-JUN-1995; 95US-00478465.
XX
XX 06-OCT-1993; 93US-00133803.
XX 06-OCT-1994; 94US-00318905.
XX (ICOS-) ICOS CORP.
XX Gray P, Tjoelker LW, Trong HL, Cousens LS, Wilder CL;
PI Eberhardt CB;
XX
XX WPI; 1997-153573/14.
DR N-PSDB; AAT63701.
XX
XX Detection of platelet-activating factor acetylhydrolase gene mutation -
PT by restriction length polymorphism analysis.
XX
XX Example 3; Col 33-38; 43pp; English.
XX
CC This sequence is that of human platelet-activating factor acetyl-
CC hydrolase (PAF-AH). The claimed method of the invention detects a
CC mutation (which results in a V279F substitution) in the PAF-AH gene, and
CC comprises performing a restriction fragment length polymorphism analysis
CC and differentiating between wild-type and mutant alleles on the basis of
CC the number of restriction sites. The method is useful for diagnosis of
CC inherited PAF-AH deficiency, which has been correlated with severe
CC respiratory symptoms in asthmatic children. Recombinant PAF-AH can be
CC used to treat inflammatory conditions. (Updated on 25-MAR-2003 to correct
CC PF field.)
XX
SQ Sequence 441 AA;

Query Match 99.6%; Score 908; DB 2; Length 441;
Best Local Similarity 99.4%; Pred. No. 7.4e-98;
Matches 170; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHSPGGATVIQTISEDQRFRCGIALDAWMPPLGDEVYSRIPOPLFFINSEYFOYPANIIK 60
DB 271 GHSPGGATVIQTISEDQRFRCGIALDAWMPPLGDEVYSRIPOPLFFINSEYFOYPANIIK 330
QY 61 MKKCYSPDKERKMTITIGSVHQNFADEFTATGKIIGHMLKLGKIDSNVAIDLNSKASLA 120
DB 331 MKKCYSPDKERKMTITIGSVHQNFADEFTATGKIIGHMLKLGKIDSNVAIDLNSKASLA 390
QY 121 FLQKHLGLHKDFQDQWDCLEGGDENLIPGNTNTNOHIMLQNSSGIEKYN 171
DB 391 FLQKHLGLHKDFQDQWDCLEGGDENLIPGNTNTNOHIMLQNSSGIEKYN 441

RESULT 13
AAW26498
ID AAW26498 standard; protein; 441 AA.
AC AAW26498;
XX
XX 25-MAR-2003 (revised)
DT 05-JAN-1998 (first entry)
XX
XX Human platelet-activating factor acetylhydrolase.
DE
XX Platelet-activating factor acetylhydrolase; PAF-AH; human; inflammation;
KW asthma; pleurisy; necrotising enterocolitis;
KW adult respiratory distress syndrome; therapy.
XX
XX Homo sapiens.
XX
XX US5656431-A.
XX
XX 12-AUG-1997.

XX 07-JUN-1995; 95US-00483232.
 XX 06-OCT-1993; 93US-00133803.
 PR 06-OCT-1994; 94US-00318905.
 XX (ICOS-) ICOS CORP.
 XX Gray P, Trong HL, Tjoelker LW, Cousens LS, Wilder CL;
 PI Eberhardt CD;
 XX MPI; 1997-414580/38.
 DR N-PSDB; AAT87048.
 XX Detecting lesions in human platelet-activating factor acetylhydrolase
 gene - by comparison with defined wild-type gene sequence.
 XX Example 3; Col 47-50; 53pp; English.
 XX This polypeptide comprises human plasma platelet-activating factor
 acetylhydrolase (PAF-AH), a protein that inactivates PAF and inactivates
 oxidatively fragmented phospholipids such as products of the arachidonic
 acid cascade that mediate inflammation. Its sequence was deduced from a
 full-length cDNA clone (see AAT87048) obtained from a macrophage cDNA
 library. Mouse, dog, cattle, chicken, rat and macaque PAF-AH polypeptides
 (see AAW26500-505) have also been identified. Recombinant PAF-AH
 polypeptides can be produced in prokaryotic or eukaryotic host cells and
 used to mimic or augment normal processes of resolution of inflammation
 in vivo. Examples describe the in vivo therapeutic effect of recombinant
 PAF-AH products on acute inflammation, pleurisy, asthma, necrotizing
 enterocolitis and adult respiratory distress syndrome in animal models.
 CC (Updated on 25-MAR-2003 to correct PF field.)
 XX Sequence 441 AA;
 SQ

Query Match 99.6%; Score 908; DB 2; Length 441;
 Best Local Similarity 99.4%; Pred. No. 7.4e-98;
 Matches 170; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GHSFGGATVIQTLSEDRFCGIALDAMFPLGDEVYSRIPQPLFFINSEYFOYPANIIK 60
 DB 271 GHSFGGATVIQTLSEDRFCGIALDAMFPLGDEVYSRIPQPLFFINSEYFOYPANIIK 330
 QY 61 MKKCYSPDKERKMITIRGSHQNFADFTFATGKIIGHMLKLGKIDSNVAIDLNSKASLA 120
 DB 331 MKKCYSPDKERKMITIRGSHQNFADFTFATGKIIGHMLKLGKIDSNVAIDLNSKASLA 390
 QY 121 FLOKHLGLHKDFQDWCLEGGDENLIPGNTNTTNOHIMLQNSSGIEKYN 171
 DB 391 FLOKHLGLHKDFQDWCLEGGDENLIPGNTNTTNOHIMLQNSSGIEKYN 441

RESULT 14
 AAW38361
 ID AAW38361 standard; protein; 441 AA.
 XX AAW38361;
 AC
 XX 31-MAR-1998 (first entry)
 DT Human plasma platelet activating factor acetylhydrolase.
 DE Human; plasma platelet activating factor acetylhydrolase;
 KW monoclonal antibody; immunoassay; diagnosis; asthma; detection.
 XX Homo sapiens.
 OS US5698403-A.
 PN 16-DEC-1997.
 PD 07-JUN-1995; 95US-00483140.
 XX

PR 06-OCT-1993; 93US-00133803.
 PR 06-OCT-1994; 94US-00318905.
 XX (ICOS-) ICOS CORP.
 XX Gray P, Trong HL, Tjoelker LW, Cousens LS, Wilder CL;
 PI Eberhardt CD;
 XX MPI; 1998-051484/05.
 DR N-PSDB; AAT96127.
 XX Immunoassay for platelet activating factor acetylhydrolase, PAF-AH -
 useful to diagnose disorders associated with abnormal PAF-AH level.
 XX Claim 1; Col 35-38; 47pp; English.
 XX The present sequence was used in the development of a method for
 detecting human, mouse, canine, rat and monkey plasma platelet activating
 factor acetylhydrolases (PAF-AH). The method comprises contacting serum
 with PAF-AH specific monoclonal antibody (MAB) to form a PAF-AH/MAB
 complex, and detecting the complex. The method can be used to diagnose
 disorders associated with abnormal PAF-AH levels, and to monitor therapy
 of such disorders. Plasma PAF-AH deficiency has been correlated with
 severe respiratory symptoms in asthmatic children who appear to have
 inherited the deficiency in an autosomal recessive manner
 XX Sequence 441 AA;
 SQ

Query Match 99.6%; Score 908; DB 2; Length 441;
 Best Local Similarity 99.4%; Pred. No. 7.4e-98;
 Matches 170; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GHSFGGATVIQTLSEDRFCGIALDAMFPLGDEVYSRIPQPLFFINSEYFOYPANIIK 60
 DB 271 GHSFGGATVIQTLSEDRFCGIALDAMFPLGDEVYSRIPQPLFFINSEYFOYPANIIK 330
 QY 61 MKKCYSPDKERKMITIRGSHQNFADFTFATGKIIGHMLKLGKIDSNVAIDLNSKASLA 120
 DB 331 MKKCYSPDKERKMITIRGSHQNFADFTFATGKIIGHMLKLGKIDSNVAIDLNSKASLA 390
 QY 121 FLOKHLGLHKDFQDWCLEGGDENLIPGNTNTTNOHIMLQNSSGIEKYN 171
 DB 391 FLOKHLGLHKDFQDWCLEGGDENLIPGNTNTTNOHIMLQNSSGIEKYN 441

RESULT 15
 AAW96334
 ID AAW96334 standard; protein; 441 AA.
 XX AAW96334;
 AC
 XX 28-JUN-1999 (first entry)
 DT Human plasma platelet-activating factor acetylhydrolase (PAF-AH).
 DE Plasma platelet activating factor acetylhydrolase; PAF-AH; PAF;
 KW platelet activating factor; inflammation; treatment; hydrolysis;
 KW augmentation; pleurisy; asthma; rhinitis; necrotizing enterocolitis;
 KW acute respiratory distress syndrome; pancreatitis; neurological disease;
 KW HIV; human immunodeficiency virus.
 XX Homo sapiens.
 OS WO9909147-A1.
 PN 25-FEB-1999.
 PD 13-AUG-1997; 97WO-US014212.
 XX 13-AUG-1997; 97WO-US014212.
 XX (ICOS-) ICOS CORP.
 PA

PI Cousens LS, Eberhardt CD, Gray P, Trong HL, Tjoelker LW;
 PI Wilder CL;
 XX
 CC WPI; 1999-181028/15.
 DR N-PSDB; AAX08463.
 XX
 CC
 PT New truncated human platelet-activating factor acetylhydrolase and its
 PT encoding polynucleotides - useful for regulating inflammatory events.
 XX
 PS Claim 1; Page 97-98; 136pp; English.
 XX
 CC Plasma platelet-activating factor acetylhydrolase (PAF-AH) can be used to
 CC inactivate the pathological effects of PAF. Pathological conditions which
 CC can be treated include pleurisy, asthma, rhinitis, necrotizing
 CC enterocolitis, acute respiratory distress syndrome, acute pancreatitis or
 CC neurological disease associated with HIV infection. Identification and
 CC isolation of polynucleotide sequences encoding human plasma PAF-AH allows
 CC the recombinant production of PAF-AH. This makes possible the use of
 CC exogenous PAF-AH to mimic or augment normal processes of resolution of
 CC inflammation in vivo. PAF inactivation occurs by hydrolysis of the PAF sn
 CC -2 acetyl group by PAF-AH. PAF-AH also metabolises oxidatively fragmented
 CC phospholipids such as products of the arachidonic acid cascade which
 CC mediate inflammation. Administration of PAF-AH is advantageous to
 CC administering PAF receptor antagonists since PAF-AH is a product normally
 CC found in plasma. Because PAF receptor antagonists are structurally
 CC related to PAF they competitively inhibit native PAF-AH activity.
 CC Treatment with recombinant PAF-AH would augment endogenous PAF-AH
 CC activity and compensate for any inactivated endogenous enzyme
 XX
 SQ Sequence 441 AA;

Query Match 99.6%; Score 908; DB 2; Length 441;
 Best Local Similarity 99.4%; Pred. No. 7.4e-98;
 Matches 170; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 GHSFGGATVIOTLSEDRFCGIALDAWMPPLGDEVYSRIPOPLFFINSEYFQYPAIIK 60
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 Qy 61 MKKCYSPDKERKMITIRGSVHONFADFTFATGKIIGHMLKLGDIIDNSNAIDLSNKLASLA 120
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 Qy 121 FLQKHGLHKDFQWDCLIEGDDENLIPGTNTNTNOHIMLQNSSGIEKYN 171
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 Job time : 65.2647 secs

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OM protein - protein search, using sw model

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Perfect score: 912

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Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	908	99.6	441	1	US-08-483-140-8
5	908	99.6	441	2	US-08-485-938A-8
6	908	99.6	441	2	US-08-910-041-8
7	908	99.6	441	3	US-09-328-474-8
8	908	99.6	441	3	US-09-100-546-8
9	908	99.6	441	3	US-09-010-715-8
10	908	99.6	441	3	US-09-577-758-8
11	776	85.1	444	2	US-08-485-938A-33
12	749	82.1	444	1	US-08-483-140-28
13	749	82.1	444	2	US-08-485-938A-32
14	672	73.7	171	1	US-08-483-140-29
15	672	73.7	171	2	US-08-485-938A-35
16	592	64.9	440	1	US-08-483-140-27
17	592	64.9	440	2	US-08-485-938A-31
18	537.5	58.9	422	2	US-08-485-938A-34
19	355	38.9	392	2	US-08-886-152-3
20	355	38.9	392	3	US-09-196-222-3
21	335	36.7	392	2	US-08-886-152-1
22	335	36.7	392	3	US-09-196-222-1
23	186	20.4	37	2	US-08-557-892-1
24	186	20.4	37	2	US-08-387-858A-1
25	186	20.4	37	3	US-09-294-384B-1
26	186	20.4	37	3	US-08-717-079-1
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30	170	18.6	30	3	US-08-717-079-2	Sequence 2, Appli
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33	104	11.4	20	3	US-09-294-384B-11	Sequence 11, Appl
34	104	11.4	20	3	US-08-717-079-11	Sequence 11, Appl
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37	104	11.4	27	3	US-09-294-384B-3	Sequence 3, Appli
38	104	11.4	27	3	US-08-717-079-3	Sequence 3, Appli
39	78	8.6	777	4	US-09-270-767-46717	Sequence 46717, A
40	77.5	8.5	321	4	US-09-543-681A-7186	Sequence 7186, Ap
41	77	8.4	460	4	US-09-248-796A-18517	Sequence 18517, A
42	75.5	8.3	435	4	US-09-949-016-7141	Sequence 7141, Ap
43	75.5	8.3	989	4	US-09-079-030-218	Sequence 218, App
44	75	8.2	317	4	US-09-634-238-383	Sequence 383, App
45	75	8.2	317	4	US-09-634-238-413	Sequence 413, App

ALIGNMENTS

RESULT 1
US-08-470-187-8
; Sequence 8, Application US/08470187
; Patent No. 5532152
; GENERAL INFORMATION:
; APPLICANT: Cousens, Lawrence S.
; APPLICANT: Eberhardt, Christine E.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor Acetyl
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gertein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/470,187
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5532152and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31672
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3658
; INFORMATION FOR SEQ ID NO:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 441 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-470-187-8
Query Match 99.6%; Score 908; DB 1; Length 441;
Best Local Similarity 99.4%; Pred. No. 8.8e-103;

Matches 170; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GHSFGGATVIOTLSEDRFCGIALDAWMFPLGDEVYSRIPQPLFFINSEYFOYPANIIK 60
Db 271 GHSFGGATVIOTLSEDRFCGIALDAWMFPLGDEVYSRIPQPLFFINSEYFOYPANIIK 330
Qy 61 MKKCYSPDKERKMITIRGSHVQNFADFTFATGKIIGHMLKLGKIDSNVAIDLNSKASLA 120
Db 331 MKKCYSPDKERKMITIRGSHVQNFADFTFATGKIIGHMLKLGKIDSNVAIDLNSKASLA 390
Qy 121 FLOKHLGLHKDFDQWDCLEGGDENLIPGTNTNTNQHIMLQNSSGIEKYN 171
Db 391 FLOKHLGLHKDFDQWDCLEGGDENLIPGTNTNTNQHIMLQNSSGIEKYN 441

RESULT 2
US-08-318-905-8
; Sequence 8, Application US/08318905
; Patent No. 5641669
; GENERAL INFORMATION:
; APPLICANT: Cousins, Lawrence S.
; APPLICANT: Eberhardt, Christine D.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Le Trong, Hai
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor Acetyl
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/318,905
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 6-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5641669and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 32205
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3658
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 441 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-318-905-8

Query Match 99.6%; Score 908; DB 1; Length 441;
Best Local Similarity 99.4%; Pred. No. 8.8e-103;
Matches 170; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GHSFGGATVIOTLSEDRFCGIALDAWMFPLGDEVYSRIPQPLFFINSEYFOYPANIIK 60
Db 271 GHSFGGATVIOTLSEDRFCGIALDAWMFPLGDEVYSRIPQPLFFINSEYFOYPANIIK 330
Qy 61 MKKCYSPDKERKMITIRGSHVQNFADFTFATGKIIGHMLKLGKIDSNVAIDLNSKASLA 120

Db 331 MKKCYSPDKERKMITIRGSHVQNFADFTFATGKIIGHMLKLGKIDSNVAIDLNSKASLA 390
Qy 121 FLOKHLGLHKDFDQWDCLEGGDENLIPGTNTNTNQHIMLQNSSGIEKYN 171
Db 391 FLOKHLGLHKDFDQWDCLEGGDENLIPGTNTNTNQHIMLQNSSGIEKYN 441

RESULT 3
US-08-483-232-8
; Sequence 8, Application US/08483232
; Patent No. 5656431
; GENERAL INFORMATION:
; APPLICANT: Cousins, Lawrence S.
; APPLICANT: Eberhardt, Christine D.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Le Trong, Hai
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,232
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/318,905
; FILING DATE: 06-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 06-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5656431and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/32689
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3658
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 441 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-483-232-8

Query Match 99.6%; Score 908; DB 1; Length 441;
Best Local Similarity 99.4%; Pred. No. 8.8e-103;
Matches 170; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GHSFGGATVIOTLSEDRFCGIALDAWMFPLGDEVYSRIPQPLFFINSEYFOYPANIIK 60
Db 271 GHSFGGATVIOTLSEDRFCGIALDAWMFPLGDEVYSRIPQPLFFINSEYFOYPANIIK 330
Qy 61 MKKCYSPDKERKMITIRGSHVQNFADFTFATGKIIGHMLKLGKIDSNVAIDLNSKASLA 120
Db 331 MKKCYSPDKERKMITIRGSHVQNFADFTFATGKIIGHMLKLGKIDSNVAIDLNSKASLA 390
Qy 121 FLOKHLGLHKDFDQWDCLEGGDENLIPGTNTNTNQHIMLQNSSGIEKYN 171

Db 391 FLOKHLGKDFDQWDCLEGGDENLPGTNTNQHIMLQNSSGIEKN 441
|||||

RESULT 4
US-08-483-140-8
; Sequence 8, Application US/08483140
; Patent No. 5698403
; GENERAL INFORMATION:

;; APPLICANT: ICOS Corporation
;; TITLE OF INVENTION: Platelet-Activating Factor Acetyl
;; TITLE OF INVENTION: Hydrolase
;; NUMBER OF SEQUENCES: 30
;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
;; STREET: 6300 Sears Tower, 233 South Wacker Drive
;; CITY: Chicago
;; STATE: Illinois
;; COUNTRY: USA
;; ZIP: 60606

;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25

;; CURRENT APPLICATION NUMBER: US/08/483,140
;; FILING DATE:
;; CLASSIFICATION: 435

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/318,905
;; FILING DATE: 6-OCT-1994
;; PRIOR APPLICATION NUMBER:

;; APPLICATION NUMBER: US 08/133,803
;; FILING DATE: 6-OCT-1993
;; ATTORNEY/AGENT INFORMATION:

;; NAME: No. 5698403and, Greta E.
;; REGISTRATION NUMBER: 35,302
;; REFERENCE/DOCKET NUMBER: 32781
;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: (312) 474-6300
;; TELEFAX: (312) 474-0448
;; TELEX: 25-3658

;; INFORMATION FOR SEQ ID NO: 8:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 441 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-483-140-8

Query Match 99.6%; Score 908; DB 1; Length 441;
Best Local Similarity 99.4%; Pred. No. 8.8e-103;
Matches 170; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GHSFGGATVIQTLSEDRFCGIALDAMWPLGDEVYSRIPOPLFFINSEYFOYPANIIK 60
Db 271 GHSFGGATVIQTLSEDRFCGIALDAMWPLGDEVYSRIPOPLFFINSEYFOYPANIIK 330

Qy 61 MKKCYSPDKERKMTIRGSHVQNFADFTFATGKIIGHMLKLKGDIDNSNAIDLNSKASLA 120
Db 331 MKKCYSPDKERKMTIRGSHVQNFADFTFATGKIIGHMLKLKGDIDNSNAIDLNSKASLA 390

Qy 121 FLOKHLGKDFDQWDCLEGGDENLPGTNTNQHIMLQNSSGIEKN 171
Db 391 FLOKHLGKDFDQWDCLEGGDENLPGTNTNQHIMLQNSSGIEKN 441
|||||

RESULT 5
US-08-485-938A-8
; Sequence 8, Application US/08485938A
; Patent No. 5647088
; GENERAL INFORMATION:

;; APPLICANT: Cousens, Lawrence S.
;; APPLICANT: Eberhardt, Christine D.
;; APPLICANT: Gray, Patrick W.
;; APPLICANT: Le Trong, Hai
;; APPLICANT: Tjoelker, Larry W.
;; APPLICANT: Wilder, Cheryl L.
;; TITLE OF INVENTION: Platelet-Activating Factor
;; TITLE OF INVENTION: Acetylhydrolase
;; NUMBER OF SEQUENCES: 36
;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
;; STREET: 6300 Sears Tower, 233 South Wacker Drive
;; CITY: Chicago
;; STATE: Illinois
;; COUNTRY: United States of America
;; ZIP: 60606-6402

;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/485,938A
;; FILING DATE:
;; CLASSIFICATION: 435

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/318,905
;; FILING DATE: 06-OCT-1994
;; PRIOR APPLICATION NUMBER:

;; APPLICATION NUMBER: US 08/133,803
;; FILING DATE: 06-OCT-1993
;; ATTORNEY/AGENT INFORMATION:

;; NAME: No. 5847088and, Greta E.
;; REGISTRATION NUMBER: 35,302
;; REFERENCE/DOCKET NUMBER: 27866/32792
;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: (312) 474-6300
;; TELEFAX: (312) 474-0448
;; TELEX: 25-3658

;; INFORMATION FOR SEQ ID NO: 8:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 441 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-485-938A-8

Query Match 99.6%; Score 908; DB 2; Length 441;
Best Local Similarity 99.4%; Pred. No. 8.8e-103;
Matches 170; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GHSFGGATVIQTLSEDRFCGIALDAMWPLGDEVYSRIPOPLFFINSEYFOYPANIIK 60
Db 271 GHSFGGATVIQTLSEDRFCGIALDAMWPLGDEVYSRIPOPLFFINSEYFOYPANIIK 330

Qy 61 MKKCYSPDKERKMTIRGSHVQNFADFTFATGKIIGHMLKLKGDIDNSNAIDLNSKASLA 120
Db 331 MKKCYSPDKERKMTIRGSHVQNFADFTFATGKIIGHMLKLKGDIDNSNAIDLNSKASLA 390

Qy 121 FLOKHLGKDFDQWDCLEGGDENLPGTNTNQHIMLQNSSGIEKN 171
Db 391 FLOKHLGKDFDQWDCLEGGDENLPGTNTNQHIMLQNSSGIEKN 441
|||||

RESULT 6
US-08-910-041-8
; Sequence 8, Application US/08910041
; Patent No. 5977308
; GENERAL INFORMATION:
;; APPLICANT: Cousens, Lawrence S.
;; APPLICANT: Eberhardt, Christine D.
;; APPLICANT: Gray, Patrick W.
;; APPLICANT: Le Trong, Hai

; APPLICANT: Tjoelker, Larry W.
 ; APPLICANT: Wilder, Cheryl L.
 ; TITLE OF INVENTION: Platelet-Activating Factor
 ; TITLE OF INVENTION: Acetylhydrolase
 ; NUMBER OF SEQUENCES: 30
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 ; STREET: 6300 Sears Tower, 233 South Wacker Drive
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: United States of America
 ; ZIP: 60606-6402
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/910,041
 ; FILING DATE:
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/483,232
 ; FILING DATE: 07-JUN-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/318,905
 ; FILING DATE: 06-OCT-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/133,803
 ; FILING DATE: 06-OCT-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Rin-Laures, Li-Hsien
 ; REGISTRATION NUMBER: 33,547
 ; REFERENCE/DOCKET NUMBER: 27866/34026
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (312) 474-6300
 ; TELEFAX: (312) 474-0448
 ; TELEX: 25-3658
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 441 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ;
 ; US-08-910-041-8

Query Match 99.6%; Score 908; DB 2; Length 441;
 Best Local Similarity 99.4%; Pred. No. 8.8e-103;
 Matches 170; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GHSFGGATVIQTLSQDQRFRCGIALDAMWPLGDEVYSRIPQLFFINSEYFOYPANIIK 60
 DB 271 GHSFGGATVIQTLSQDQRFRCGIALDAMWPLGDEVYSRIPQLFFINSEYFOYPANIIK 330
 QY 61 MKCYSPPDKERKMTIRGSHVQNFADFTATGKIIGHMLKLGKIDSNVAIDLSNKASLA 120
 DB 331 MKCYSPPDKERKMTIRGSHVQNFADFTATGKIIGHMLKLGKIDSNVAIDLSNKASLA 390
 QY 121 FLQKHLGLHKDFQDWCCLIEGDDENLIPGNTNTNQHIMLQNSSGIEKYN 171
 DB 391 FLQKHLGLHKDFQDWCCLIEGDDENLIPGNTNTNQHIMLQNSSGIEKYN 441

RESULT 7
 US-09-328-474-8
 ; Sequence 8, Application US/09328474
 ; Patent No. 6045794
 ; GENERAL INFORMATION:
 ; APPLICANT: Cousens, Lawrence S.
 ; APPLICANT: Eberhardt, Christine D.
 ; APPLICANT: Gray, Patrick W.
 ; APPLICANT: Le Trong, Hai
 ; APPLICANT: Tjoelker, Larry W.

; APPLICANT: Wilder, Cheryl L.
 ; TITLE OF INVENTION: Platelet-Activating Factor
 ; TITLE OF INVENTION: Acetylhydrolase
 ; NUMBER OF SEQUENCES: 30
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 ; STREET: 6300 Sears Tower, 233 South Wacker Drive
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: United States of America
 ; ZIP: 60606-6402
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/328,474
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/483,232
 ; FILING DATE: 07-JUN-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/318,905
 ; FILING DATE: 06-OCT-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/133,803
 ; FILING DATE: 06-OCT-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Rin-Laures, Li-Hsien
 ; REGISTRATION NUMBER: 33,547
 ; REFERENCE/DOCKET NUMBER: 27866/34026
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (312) 474-6300
 ; TELEFAX: (312) 474-0448
 ; TELEX: 25-3658
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 441 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ;
 ; US-09-328-474-8

Query Match 99.6%; Score 908; DB 3; Length 441;
 Best Local Similarity 99.4%; Pred. No. 8.8e-103;
 Matches 170; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GHSFGGATVIQTLSQDQRFRCGIALDAMWPLGDEVYSRIPQLFFINSEYFOYPANIIK 60
 DB 271 GHSFGGATVIQTLSQDQRFRCGIALDAMWPLGDEVYSRIPQLFFINSEYFOYPANIIK 330
 QY 61 MKCYSPPDKERKMTIRGSHVQNFADFTATGKIIGHMLKLGKIDSNVAIDLSNKASLA 120
 DB 331 MKCYSPPDKERKMTIRGSHVQNFADFTATGKIIGHMLKLGKIDSNVAIDLSNKASLA 390
 QY 121 FLQKHLGLHKDFQDWCCLIEGDDENLIPGNTNTNQHIMLQNSSGIEKYN 171
 DB 391 FLQKHLGLHKDFQDWCCLIEGDDENLIPGNTNTNQHIMLQNSSGIEKYN 441

RESULT 8
 US-09-100-546-8
 ; Sequence 8, Application US/09100546
 ; Patent No. 6089836
 ; GENERAL INFORMATION:
 ; APPLICANT: Cousens, Lawrence S.
 ; APPLICANT: Eberhardt, Christine D.
 ; APPLICANT: Gray, Patrick W.
 ; APPLICANT: Le Trong, Hai
 ; APPLICANT: Tjoelker, Larry W.
 ; APPLICANT: Wilder, Cheryl L.

;; TITLE OF INVENTION: Platelet-Activating Factor
;; TITLE OF INVENTION: Acetylhydrolase
;; NUMBER OF SEQUENCES: 30
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
;; STREET: 6300 Sears Tower, 233 South Wacker Drive
;; CITY: Chicago
;; STATE: Illinois
;; COUNTRY: United States of America
;; ZIP: 60606-6402
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/100,546
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/09/010,715
;; FILING DATE:
;; APPLICATION NUMBER: US 08/318,905
;; FILING DATE: 06-OCT-1994
;; APPLICATION NUMBER: US 08/133,803
;; FILING DATE: 06-OCT-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: No. 6099836and, Greta E.
;; REGISTRATION NUMBER: 35,302
;; REFERENCE/DOCKET NUMBER: 27866/32793
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (312) 474-6300
;; TELEFAX: (312) 474-0448
;; TELEX: 25-3658
;; INFORMATION FOR SEQ ID NO: 8:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 441 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-09-100-546-8

Query Match 99.6%; Score 908; DB 3; Length 441;
Best Local Similarity 99.4%; Pred. No. 8.8e-103;
Matches 170; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GHSFGGATVIQTLSQDQRCGIALDAWMPPLGDEVYSRIPQPLFFINSEYFQYPAIIK 60
Db 271 GHSFGGATVIQTLSQDQRCGIALDAWMPPLGDEVYSRIPQPLFFINSEYFQYPAIIK 330

Qy 61 MKCYSPDKERKMTIRGSHQNFADFTFATGKIIGHMLKLGKIDSNAAIDLNSKASLA 120
Db 331 MKCYSPDKERKMTIRGSHQNFADFTFATGKIIGHMLKLGKIDSNVAIDLNSKASLA 390

Qy 121 FLQKHLGKDFQDQWCLIEGDDENLIPGTNTNTNQHIMLQNSSGIEKN 171
Db 391 FLQKHLGKDFQDQWCLIEGDDENLIPGTNTNTNQHIMLQNSSGIEKN 441

RESULT 9
US-09-010-715-8
; Sequence 8, Application US/09010715
; Patent No. 6146625
; GENERAL INFORMATION:
; APPLICANT: Cousens, Lawrence S.
; APPLICANT: Eberhardt, Christine D.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Le Trong, Hai
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor
; TITLE OF INVENTION: Acetylhydrolase

;; NUMBER OF SEQUENCES: 30
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
;; STREET: 6300 Sears Tower, 233 South Wacker Drive
;; CITY: Chicago
;; STATE: Illinois
;; COUNTRY: United States of America
;; ZIP: 60606-6402
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/010,715
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/318,905
;; FILING DATE: 06-OCT-1994
;; APPLICATION NUMBER: US 08/133,803
;; FILING DATE: 06-OCT-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: No. 6146625and, Greta E.
;; REGISTRATION NUMBER: 35,302
;; REFERENCE/DOCKET NUMBER: 27866/32793
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (312) 474-6300
;; TELEFAX: (312) 474-0448
;; TELEX: 25-3658
;; INFORMATION FOR SEQ ID NO: 8:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 441 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-09-010-715-8

Query Match 99.6%; Score 908; DB 3; Length 441;
Best Local Similarity 99.4%; Pred. No. 8.8e-103;
Matches 170; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GHSFGGATVIQTLSQDQRCGIALDAWMPPLGDEVYSRIPQPLFFINSEYFQYPAIIK 60
Db 271 GHSFGGATVIQTLSQDQRCGIALDAWMPPLGDEVYSRIPQPLFFINSEYFQYPAIIK 330

Qy 61 MKCYSPDKERKMTIRGSHQNFADFTFATGKIIGHMLKLGKIDSNAAIDLNSKASLA 120
Db 331 MKCYSPDKERKMTIRGSHQNFADFTFATGKIIGHMLKLGKIDSNVAIDLNSKASLA 390

Qy 121 FLQKHLGKDFQDQWCLIEGDDENLIPGTNTNTNQHIMLQNSSGIEKN 171
Db 391 FLQKHLGKDFQDQWCLIEGDDENLIPGTNTNTNQHIMLQNSSGIEKN 441

RESULT 10
US-09-577-758-8
; Sequence 8, Application US/09577758
; Patent No. 6203790
; GENERAL INFORMATION:
; APPLICANT: Cousens, Lawrence S.
; APPLICANT: Eberhardt, Christine D.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Le Trong, Hai
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor
; TITLE OF INVENTION: Acetylhydrolase
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive

;; CITY: Chicago
;; STATE: Illinois
;; COUNTRY: United States of America
;; ZIP: 60606-6402
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/577,758
;; FILING DATE:
;; CLASSIFICATION:
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 09/010,715
;; FILING DATE:
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/133,803
;; FILING DATE: 06-OCT-1993
;;
;; ATTORNEY/AGENT INFORMATION:
;; NAME: No. 6203790and, Greta E.
;; REGISTRATION NUMBER: 35,302
;; REFERENCE/DOCKET NUMBER: 27866/32793
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (312) 474-6300
;; TELEFAX: (312) 474-0448
;; TELEX: 25-3658
;;
;; INFORMATION FOR SEQ ID NO: 8:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 441 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;;
;; US-09-577-758-8

Query Match 99.68; Score 908; DB 3; Length 441;
Best Local Similarity 99.48; Pred. No. 8.8e-103;
Matches 170; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHSFGGATVIQTLSQDQRCGIALDAWMPFLGDEVYSRIPQPLFFINSEYFOYVANI 60
DB 271 GHSFGGATVIQTLSQDQRCGIALDAWMPFLGDEVYSRIPQPLFFINSEYFOYVANI 330

QY 61 MKKCYSPDKERKMITIRGSHVQNFADFTATGKIIGHMLKLGKIDSDNAIDLSNKASLA 120
DB 331 MKKCYSPDKERKMITIRGSHVQNFADFTATGKIIGHMLKLGKIDSDNAIDLSNKASLA 390

QY 121 FLOKHLGLHDKDFQWDCLEIGDDENLIPGNTNTTNOHIMLQNSSGIEKYN 171
DB 391 FLOKHLGLHDKDFQWDCLEIGDDENLIPGNTNTTNOHIMLQNSSGIEKYN 441

RESULT 11
US-08-485-938A-33
; Sequence 33, Application US/08485938A
; Patent No. 5847088
; GENERAL INFORMATION:
; APPLICANT: Cousens, Lawrence S.
; APPLICANT: Eberhardt, Christine D.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Le Trong, Hai
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402

;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/485,938A
;; FILING DATE:
;; CLASSIFICATION: 435
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/318,905
;; FILING DATE: 06-OCT-1994
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/133,803
;; FILING DATE: 06-OCT-1993
;;
;; ATTORNEY/AGENT INFORMATION:
;; NAME: No. 5847088and, Greta E.
;; REGISTRATION NUMBER: 35,302
;; REFERENCE/DOCKET NUMBER: 27866/32792
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (312) 474-6300
;; TELEFAX: (312) 474-0448
;; TELEX: 25-3658
;;
;; INFORMATION FOR SEQ ID NO: 33:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 444 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;;
;; US-08-485-938A-33

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Best Local Similarity 84.2%; Pred. No. 1.5e-86;
Matches 144; Conservative 12; Mismatches 15; Indels 0; Gaps 0;

QY 1 GHSFGGATVIQTLSQDQRCGIALDAWMPFLGDEVYSRIPQPLFFINSEYFOYVANI 60
DB 272 GHSFGGATVIQTLSQDQRCGIALDAWMPFLGDEVYSRIPQPLFFINSEYFOYVANI 331

QY 61 MKKCYSPDKERKMITIRGSHVQNFADFTATGKIIGHMLKLGKIDSDNAIDLSNKASLA 120
DB 332 MKKCYSPDKERKMITIRGSHVQNFADFTATGKIIGHMLKLGKIDSDNAIDLSNKASLA 391

QY 121 FLOKHLGLHDKDFQWDCLEIGDDENLIPGNTNTTNOHIMLQNSSGIEKYN 171
DB 392 FLOKHLGLHDKDFQWDCLEIGDDENLIPGNTNTTNOHIMLQNSSGIEKYN 442

RESULT 12
US-08-483-140-28
; Sequence 28, Application US/08483140
; Patent No. 5698403
; GENERAL INFORMATION:
; APPLICANT: ICOS Corporation
; TITLE OF INVENTION: Platelet-Activating Factor Acetyl
; TITLE OF INVENTION: Hydrolase
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,140
; FILING DATE:
; CLASSIFICATION: 435

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/318,905
; FILING DATE: 6-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 6-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5698403and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 32781
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-0448
; TELEFAX: (312) 474-0448
; TELEX: 25-3658
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 444 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-483-140-28

Query Match      82.1%; Score 749; DB 1; Length 444;
Best Local Similarity 82.5%; Pred. No. 3.1e-83;
Matches 141; Conservative 8; Mismatches 22; Indels 0; Gaps 0;

Qy 1 GHSFGATVIQTLSEDRFCGIALDAWMPFLGDEVYSRIPQPLFFINSEYFOYPANIK 60
Db 272 GHSFGATVQLALSEDQRFCGIALDAWMLPLDDAIYSRIPQPLFFINSEYFOYPANIK 331
Qy 61 MKKCYSPDKERKMTIRGSHQNFADFTFATGKIIGHMLKLKGDIDNSNAIDLKASLA 120
Db 332 MKKCYSPDKERKMTIRGSHQNFADFTFATGKIIGHMLKLKGDIDNSNAIDLKASLA 391
Qy 121 FLOKHLGLKDFDQWCLIEGDDENLPGTNTNTHOHIMLQNSSGIEKYN 171
Db 392 FLOKHLGLKDFDQWCLIEGDDENLPGTNTNTHOHIMLQNSSGIEKYN 442

RESULT 13
US-08-485-938A-32
; Sequence 32, Application US/08485938A
; Patent No. 5847088
; GENERAL INFORMATION:
; APPLICANT: Cousins, Lawrence S.
; APPLICANT: Eberhardt, Christine D.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Le Trong, Hai
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,938A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/318,905
; FILING DATE: 6-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 6-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5698403and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 32781
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-0448
; TELEFAX: (312) 474-0448
; TELEX: 25-3658
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 444 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-483-140-28

Query Match      82.1%; Score 749; DB 2; Length 444;
Best Local Similarity 82.5%; Pred. No. 3.1e-83;
Matches 141; Conservative 8; Mismatches 22; Indels 0; Gaps 0;

Qy 1 GHSFGATVIQTLSEDRFCGIALDAWMPFLGDEVYSRIPQPLFFINSEYFOYPANIK 60
Db 272 GHSFGATVQLALSEDQRFCGIALDAWMLPLDDAIYSRIPQPLFFINSEYFOYPANIK 331
Qy 61 MKKCYSPDKERKMTIRGSHQNFADFTFATGKIIGHMLKLKGDIDNSNAIDLKASLA 120
Db 332 MKKCYSPDKERKMTIRGSHQNFADFTFATGKIIGHMLKLKGDIDNSNAIDLKASLA 391
Qy 121 FLOKHLGLKDFDQWCLIEGDDENLPGTNTNTHOHIMLQNSSGIEKYN 171
Db 392 FLOKHLGLKDFDQWCLIEGDDENLPGTNTNTHOHIMLQNSSGIEKYN 442

RESULT 14
US-08-483-140-29
; Sequence 29, Application US/08483140
; Patent No. 5698403
; GENERAL INFORMATION:
; APPLICANT: ICOS Corporation
; TITLE OF INVENTION: Platelet-Activating Factor Acetyl
; TITLE OF INVENTION: Hydrolase
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/483,140
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/318,905
; FILING DATE: 6-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 6-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5698403and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 32781
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-0448
; TELEFAX: (312) 474-0448
; TELEX: 25-3658
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 444 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-485-938A-32
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; TELEX: 25-3658
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 171 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-483-140-29

Query Match      73.7%; Score 672; DB 1; Length 171;
Best Local Similarity 73.7%; Pred. No. 2.3e-74;
Matches 126; Conservative 14; Mismatches 31; Indels 0; Gaps 0;

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DB 1 GHSFGGATVFOALSEDOQRFCGIALDPMWPFVSEELYSRVQPLFFINSAEFQPKDIAK 60
QY 61 MKKCYSPDKERKMTITIGSVHQNFADETFATGKIIGHMLKLGKIDSNAAIDLSNKASLA 120
DB 61 MKNFYQDPKERRMTITIGSVHQNFADETFATGKIIGHMLKLGKIDSNAAIDLSNKASLA 120
QY 121 FLOKHLGLHKDFDQWDCLEGGDENLIPGTNINTNQHIHMLQNSSGIEKYN 171
DB 121 FLOKHLGLHKDFDQWDCLEGGDENLIPGTNINTNQHIHMLQNSSGIEKYN 171

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RESULT 15
US-08-485-938A-35
; Sequence 35, Application US/08485938A
; Patent No. 5847088
; GENERAL INFORMATION:
; APPLICANT: Cousens, Lawrence S.
; APPLICANT: Eberhardt, Christine D.
; APPLICANT: Gray, Patrick W.
; APPLICANT: Le Trong, Hai
; APPLICANT: Tjoelker, Larry W.
; APPLICANT: Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor
; TITLE OF INVENTION: Acetylhydrolase
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,938A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/318,905
; FILING DATE: 06-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 06-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5847088and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/32792
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 171 amino acids

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 15, 2005, 10:07:52 ; Search time 51.1324 Seconds
(without alignments)
1103.088 Million cell updates/sec

Title: US-09-922-067F-14_COPY_271_441

Perfect score: 912

Sequence: 1 GHSGGATVQTLSSEDRFR.....INTNQHIMLQSSGIEKYN 171

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1396920 seqs, 329844858 residues

Total number of hits satisfying chosen parameters: 1396920

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	908	99.6	441	9	US-09-729-402-8
4	908	99.6	441	14	US-10-003-978A-8
5	908	99.6	441	14	US-10-161-127-1
6	908	99.6	441	16	US-10-755-889-278
7	355	38.9	392	10	US-09-961-253-3
8	335	36.7	392	10	US-09-961-253-1
9	186	20.4	37	9	US-09-922-067-1
10	186	20.4	37	14	US-10-173-233-1
11	186	20.4	37	14	US-10-406-156-1
12	186	20.4	384	15	US-10-369-493-5034
13	184	20.2	476	15	US-10-369-493-6760

14	170	18.6	30	9	US-09-922-067-2	Sequence 2, Appli
15	170	18.6	30	14	US-10-173-233-2	Sequence 2, Appli
16	170	18.6	30	14	US-10-406-156-2	Sequence 2, Appli
17	133	14.6	438	15	US-10-369-493-2350	Sequence 2350, Ap
18	104	11.4	20	9	US-09-922-067-11	Sequence 11, Appl
19	104	11.4	20	14	US-10-173-233-11	Sequence 11, Appl
20	104	11.4	20	14	US-10-406-156-11	Sequence 11, Appl
21	104	11.4	27	9	US-09-922-067-3	Sequence 3, Appli
22	104	11.4	27	14	US-10-173-233-3	Sequence 3, Appli
23	104	11.4	27	14	US-10-406-156-3	Sequence 3, Appli
24	93.5	10.3	439	15	US-10-354-437-112	Sequence 112, App
25	82.5	9.0	401	14	US-10-156-761-8015	Sequence 8015, Ap
26	81.5	8.9	408	15	US-10-282-122A-52450	Sequence 52450, A
27	81	8.9	521	16	US-10-686-947-250	Sequence 250, App
28	81	8.9	521	16	US-10-686-947-270	Sequence 270, App
29	81	8.9	521	16	US-10-686-947-274	Sequence 274, App
30	77	8.4	460	15	US-10-425-114-47561	Sequence 47561, A
31	76.5	8.4	483	9	US-09-888-615-79	Sequence 79, Appl
32	76.5	8.4	483	14	US-10-131-985-53	Sequence 53, Appl
33	76.5	8.4	483	17	US-10-901-417-53	Sequence 53, Appl
34	76	8.3	502	15	US-10-282-122A-54571	Sequence 54571, A
35	75.5	8.3	194	15	US-10-425-114-42047	Sequence 42047, A
36	75	8.2	273	15	US-10-369-493-11644	Sequence 11644, A
37	75	8.2	273	15	US-10-369-493-15162	Sequence 15162, A
38	75	8.2	275	15	US-10-369-493-14679	Sequence 14679, A
39	75	8.2	317	9	US-09-971-536-44	Sequence 44, Appl
40	74.5	8.2	496	9	US-09-974-592-10	Sequence 10, Appl
41	74.5	8.2	496	9	US-09-201-936-10	Sequence 10, Appl
42	74.5	8.2	496	16	US-10-636-065-225	Sequence 225, App
43	74.5	8.2	496	16	US-10-600-272-10	Sequence 10, Appl
44	74	8.1	451	9	US-09-874-923-108	Sequence 108, App
45	74	8.1	451	9	US-09-991-496-108	Sequence 108, App

ALIGNMENTS

RESULT 1

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US-10-741-601-373
; Sequence 373, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCES: CL001500
; CURRENT APPLICATION NUMBER: US/10/741.601
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 28415
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 373
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-741-601-373

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Query Match 100.0%; Score 912; DB 16; Length 441;
Best Local Similarity 100.0%; Pred. No. 7.2e-93;
Matches 171; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	271	GHSGGATVQTLSSEDRFCGIALDAWMPPLGDEVYSRIPQPLFFINSEYFQYPAIIK	330
Qy	61	MKKYSPDKERKMTTIRGSHQNFADFTFTGKIIGHMLKLGKIDISNAADLSNKASLA	120
Db	331	MKKYSPDKERKMTTIRGSHQNFADFTFTGKIIGHMLKLGKIDISNAADLSNKASLA	390
Qy	121	FLOHGLHLDKDFQWDCLEGGDENLIPGTNTNTNQHIMLQSSGIEKYN	171
Db	391	FLOHGLHLDKDFQWDCLEGGDENLIPGTNTNTNQHIMLQSSGIEKYN	441

RESULT 2
US-10-741-601-374
; Sequence 374, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C0001500
; CURRENT APPLICATION NUMBER: US/10741.601
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 26415
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 374
; LENGTH: 441
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-741-601-374

Query Match 100.0%; Score 912; DB 16; Length 441;
Best Local Similarity 100.0%; Pred. No. 7.2e-93;
Matches 171; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GHSFGGATVIQTLSQDORFCGIALDAWMPPLGDEVYSRIPQPLFFINSEYFOYPANIIK 60
Db 271 GHSFGGATVIQTLSQDORFCGIALDAWMPPLGDEVYSRIPQPLFFINSEYFOYPANIIK 330
Qy 61 MKKCYSPDKERKMITTIRGSHQNFADFTFATGKIIGHMLKLGKIDSNAAIDLSNKASLA 120
Db 331 MKKCYSPDKERKMITTIRGSHQNFADFTFATGKIIGHMLKLGKIDSNAAIDLSNKASLA 390
Qy 121 FLOKHLGHKDFQWDCLIEGDDENLIPGNTNTNQHIMLQNSSGIEKYN 171
Db 391 FLOKHLGHKDFQWDCLIEGDDENLIPGNTNTNQHIMLQNSSGIEKYN 441

RESULT 3
US-09-729-402-8
; Sequence 8, Application US/09729402
; Patent No. US20010021379A1
; GENERAL INFORMATION:
; APPLICANT: Cousens, Lawrence S.
; Eberhardt, Christine D.
; Gray, Patrick W.
; Le Trong, Hai
; Tjoelker, Larry W.
; Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/729,402
; FILING DATE: 04-Dec-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/318,905
; FILING DATE: 06-Oct-1994
; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 06-Oct-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. US20010021379Aland, Greta E.

REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/32793
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3658
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 441 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-729-402-8

Query Match 99.6%; Score 908; DB 9; Length 441;
Best Local Similarity 99.4%; Pred. No. 2e-92;
Matches 170; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GHSFGGATVIQTLSQDORFCGIALDAWMPPLGDEVYSRIPQPLFFINSEYFOYPANIIK 60
Db 271 GHSFGGATVIQTLSQDORFCGIALDAWMPPLGDEVYSRIPQPLFFINSEYFOYPANIIK 330
Qy 61 MKKCYSPDKERKMITTIRGSHQNFADFTFATGKIIGHMLKLGKIDSNAAIDLSNKASLA 120
Db 331 MKKCYSPDKERKMITTIRGSHQNFADFTFATGKIIGHMLKLGKIDSNAAIDLSNKASLA 390
Qy 121 FLOKHLGHKDFQWDCLIEGDDENLIPGNTNTNQHIMLQNSSGIEKYN 171
Db 391 FLOKHLGHKDFQWDCLIEGDDENLIPGNTNTNQHIMLQNSSGIEKYN 441

RESULT 4
US-10-003-978A-8
; Sequence 8, Application US/10003978A
; Publication No. US20030072747A1
; GENERAL INFORMATION:
; APPLICANT: Cousens, Lawrence S.
; Eberhardt, Christine D.
; Gray, Patrick W.
; Le Trong, Hai
; Tjoelker, Larry W.
; Wilder, Cheryl L.
; TITLE OF INVENTION: Platelet-Activating Factor
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, Gerstein & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6357
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/003,978A
; FILING DATE: 23-Oct-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/729,402
; FILING DATE: 04-DEC-2000
; APPLICATION NUMBER: US 09/577,758
; FILING DATE: 23-MAY-2000
; APPLICATION NUMBER: US 09/010,715
; FILING DATE: 22-JAN-1998
; APPLICATION NUMBER: US 08/480,658
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/318,905
; FILING DATE: 06-OCT-1994

```

; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 06-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. US20030072747Aland, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/37792
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 441 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-003-978A-8

Query Match          99.6%; Score 908; DB 14; Length 441;
Best Local Similarity 99.4%; Pred. No. 2e-92;
Matches 170; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GHSFGGATVIQTLSQDQFRGCIADAWMPPLGDEVYSRIPQPLFFINSEYFOYPANIIK 60
Db 271 GHSFGGATVIQTLSQDQFRGCIADAWMPPLGDEVYSRIPQPLFFINSEYFOYPANIIK 330

Qy 61 MKKCYSPDKERKMITIRGSHVQNFADFTFATGKIIGHMLKLGKIDNSNAIDLSNKASLA 120
Db 331 MKKCYSPDKERKMITIRGSHVQNFADFTFATGKIIGHMLKLGKIDNSNAIDLSNKASLA 390

Qy 121 FLOKHLGLHKDFQDWCLEGGDENLIPGTNTNTNQHIMLQNSSGIEKYN 171
Db 391 FLOKHLGLHKDFQDWCLEGGDENLIPGTNTNTNQHIMLQNSSGIEKYN 441

RESULT 5
US-10-161-127-1
; Sequence 1, Application US/10161127
; Publication No. US20030166225A1
; GENERAL INFORMATION:
; APPLICANT: Ryan, James W.
; TITLE OF INVENTION: ISOLATED GENOMIC POLYNUCLEOTIDE FRAGMENTS THAT ENCODE
; FILE REFERENCE: JR-16,001
; CURRENT APPLICATION NUMBER: US/10/161,127
; CURRENT FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: US 60/294,404
; PRIOR FILING DATE: 2001-05-30
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 441
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-161-127-1

Query Match          99.6%; Score 908; DB 14; Length 441;
Best Local Similarity 99.4%; Pred. No. 2e-92;
Matches 170; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GHSFGGATVIQTLSQDQFRGCIADAWMPPLGDEVYSRIPQPLFFINSEYFOYPANIIK 60
Db 271 GHSFGGATVIQTLSQDQFRGCIADAWMPPLGDEVYSRIPQPLFFINSEYFOYPANIIK 330

Qy 61 MKKCYSPDKERKMITIRGSHVQNFADFTFATGKIIGHMLKLGKIDNSNAIDLSNKASLA 120
Db 331 MKKCYSPDKERKMITIRGSHVQNFADFTFATGKIIGHMLKLGKIDNSNAIDLSNKASLA 390

Qy 121 FLOKHLGLHKDFQDWCLEGGDENLIPGTNTNTNQHIMLQNSSGIEKYN 171
Db 391 FLOKHLGLHKDFQDWCLEGGDENLIPGTNTNTNQHIMLQNSSGIEKYN 441

; APPLICATION NUMBER: US 08/133,803
; FILING DATE: 06-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: No. US20030072747Aland, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/37792
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 441 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-003-978A-8

Query Match          99.6%; Score 908; DB 14; Length 441;
Best Local Similarity 99.4%; Pred. No. 2e-92;
Matches 170; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GHSFGGATVIQTLSQDQFRGCIADAWMPPLGDEVYSRIPQPLFFINSEYFOYPANIIK 60
Db 271 GHSFGGATVIQTLSQDQFRGCIADAWMPPLGDEVYSRIPQPLFFINSEYFOYPANIIK 330

Qy 61 MKKCYSPDKERKMITIRGSHVQNFADFTFATGKIIGHMLKLGKIDNSNAIDLSNKASLA 120
Db 331 MKKCYSPDKERKMITIRGSHVQNFADFTFATGKIIGHMLKLGKIDNSNAIDLSNKASLA 390

Qy 121 FLOKHLGLHKDFQDWCLEGGDENLIPGTNTNTNQHIMLQNSSGIEKYN 171
Db 391 FLOKHLGLHKDFQDWCLEGGDENLIPGTNTNTNQHIMLQNSSGIEKYN 441
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RESULT 6
US-10-755-889-278
; Sequence 278, Application US/10755889
; Publication No. US20040171823A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-kB
; TITLE OF INVENTION: PATHWAY
; FILE REFERENCE: D0284 NP
; CURRENT APPLICATION NUMBER: US/10/755,889
; CURRENT FILING DATE: 2004-01-13
; PRIOR APPLICATION NUMBER: U.S. 60/440,068
; PRIOR FILING DATE: 2003-01-14
; PRIOR APPLICATION NUMBER: U.S. 60/469,757
; PRIOR FILING DATE: 2003-05-12
; NUMBER OF SEQ ID NOS: 823
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 278
; LENGTH: 441
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-755-889-278

Query Match          99.6%; Score 908; DB 16; Length 441;
Best Local Similarity 99.4%; Pred. No. 2e-92;
Matches 170; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GHSFGGATVIQTLSQDQFRGCIADAWMPPLGDEVYSRIPQPLFFINSEYFOYPANIIK 60
Db 271 GHSFGGATVIQTLSQDQFRGCIADAWMPPLGDEVYSRIPQPLFFINSEYFOYPANIIK 330

Qy 61 MKKCYSPDKERKMITIRGSHVQNFADFTFATGKIIGHMLKLGKIDNSNAIDLSNKASLA 120
Db 331 MKKCYSPDKERKMITIRGSHVQNFADFTFATGKIIGHMLKLGKIDNSNAIDLSNKASLA 390

Qy 121 FLOKHLGLHKDFQDWCLEGGDENLIPGTNTNTNQHIMLQNSSGIEKYN 171
Db 391 FLOKHLGLHKDFQDWCLEGGDENLIPGTNTNTNQHIMLQNSSGIEKYN 441

RESULT 7
US-09-961-253-3
; Sequence 3, Application US/09961253
; Publication No. US20030040093A1
; GENERAL INFORMATION:
; APPLICANT: ADACHI, HIDEKI
; TSUJIMOTO, MASAFUMI
; ARAI, HIROYUKI
; INOUE, KEIZO
; TITLE OF INVENTION: PLATELET ACTIVATING FACTOR
; ACETYLHYDROLASE, AND GENE THEREOF
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; P.C.
; STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/961,253
; FILING DATE: 25-Sep-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/196,222
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/886,152
```


;; FILING DATE: 24 June 1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Dustman, Wayne J.
;; REGISTRATION NUMBER: 33,870
;; REFERENCE/DOCKET NUMBER: P30693
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 610-270-5023
;; TELEFAX: 610-270-5090
;; TELEX: <Unknown>
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 37 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: <Unknown>
;; MOLECULE TYPE: peptide
;; TOPOLOGY: linear
;; HYPOTHETICAL: NO
;; FRAGMENT TYPE: internal
;; ORIGINAL SOURCE:
;; FEATURE:
;; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-922-067-1
Query Match 20.4%; Score 186; DB 9; Length 37;
Best Local Similarity 100.0%; Pred. No. 2.9e-13;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 98 MLKLGIDISNAADLSNKLASLAPLQKHGLHKDFDQ 134
Db 1 MLKLGIDISNAADLSNKLASLAPLQKHGLHKDFDQ 37
RESULT 10
US-10-173-233-1
; Sequence 1, Application US/10173233
; Publication No. US20030148398A1
; GENERAL INFORMATION:
; APPLICANT: MacPhee, Colin Houston
; Tew, David Graham
; Southan, Christopher Donald
; Hickey, Dierdre Mary Bernadette
; Gloger, Israel Simon
; Lawrence, Geoffrey Mark Prouse
; Rice, Simon Quentyn John
; TITLE OF INVENTION: Compounds
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/173,233
; FILING DATE: 14-Jun-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/569,899
; FILING DATE: 12-May-2000
; ATTORNEY/AGENT INFORMATION:
; NAME: Dustman, Wayne J.
; REGISTRATION NUMBER: 33,870
; REFERENCE/DOCKET NUMBER: P30693
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5023
; TELEFAX: 610-270-5090
; TELEX: <Unknown>

;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 37 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: <Unknown>
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; HYPOTHETICAL: NO
;; FRAGMENT TYPE: internal
;; ORIGINAL SOURCE:
;; FEATURE:
;; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-173-233-1
Query Match 20.4%; Score 186; DB 14; Length 37;
Best Local Similarity 100.0%; Pred. No. 2.9e-13;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 98 MLKLGIDISNAADLSNKLASLAPLQKHGLHKDFDQ 134
Db 1 MLKLGIDISNAADLSNKLASLAPLQKHGLHKDFDQ 37
RESULT 11
US-10-406-156-1
; Sequence 1, Application US/10406156
; Publication No. US20030186421A1
; GENERAL INFORMATION:
; APPLICANT: MacPhee, Colin Houston
; Tew, David Graham
; Southan, Christopher Donald
; Hickey, Dierdre Mary Bernadette
; Gloger, Israel Simon
; Lawrence, Geoffrey Mark Prouse
; Rice, Simon Quentyn John
; TITLE OF INVENTION: Compounds
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/406,156
; FILING DATE: 02-Apr-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/569,899
; FILING DATE: 12-May-2000
; APPLICATION NUMBER: 09/294,384
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Dustman, Wayne J.
; REGISTRATION NUMBER: 33,870
; REFERENCE/DOCKET NUMBER: P30693
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5023
; TELEFAX: 610-270-5090
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 37 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; HYPOTHETICAL: NO
;; FRAGMENT TYPE: internal
;; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-922-067-2

Query Match 18.6%; Score 170; DB 9; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.3e-11;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 28 WMFPLGDEVYSRIQPLFFINSEYFQYPAN 57
Db 1 WMFPLGDEVYSRIQPLFFINSEYFQYPAN 30

RESULT 15

US-10-173-233-2
; Sequence 2, Application US/10173233
; Publication No. US20030148398A1

GENERAL INFORMATION:

;; APPLICANT: MacPhee, Colin Houston
;; Tew, David Graham
;; Southan, Christopher Donald
;; Hickey, Dierdre Mary Bernadette
;; Gloger, Israel Simon
;; Lawrence, Geoffrey Mark Prouse
;; Rice, Simon Quentyn John

TITLE OF INVENTION: Compounds

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

;; ADDRESSEE: SmithKline Beecham Corporation
;; STREET: 709 Swedeland Road
;; CITY: King of Prussia
;; STATE: PA
;; COUNTRY: USA
;; ZIP: 19406

COMPUTER READABLE FORM:

;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)

CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/10/173,233
;; FILING DATE: 14-Jun-2002
;; CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: US/09/569,899
;; FILING DATE: 12-May-2000

ATTORNEY/AGENT INFORMATION:

;; NAME: Dustman, Wayne J.
;; REGISTRATION NUMBER: 33,870
;; REFERENCE/DOCKET NUMBER: P30693
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 610-270-5023
;; TELEFAX: 610-270-5090
;; TELEX: <Unknown>

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

;; LENGTH: 30 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; HYPOTHETICAL: NO

FRAGMENT TYPE: internal

SEQUENCE DESCRIPTION: SEQ ID NO: 2:

US-10-173-233-2

Query Match 18.6%; Score 170; DB 14; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.3e-11;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 28 WMFPLGDEVYSRIQPLFFINSEYFQYPAN 57

Db 1 WMFPLGDEVYSRIQPLFFINSEYFQYPAN 30

Search completed: March 15, 2005, 10:25:10
Job time : 52.1324 secs

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Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	908	99.6	441	2	S60247	platelet-activatin
2	627.5	68.8	436	2	JC5021	platelet-activatin
3	186	20.4	384	2	T23756	hypothetical prote
4	184	20.2	476	2	T28936	hypothetical prote
5	133	14.6	438	2	T39268	hypothetical prote
6	129.5	14.2	450	2	G83740	hypothetical prote
7	84	9.2	317	2	D64220	methyltransferase
8	83	9.1	382	2	S56151	tubulin alpha chai
9	82.5	9.0	1154	2	A83118	protein F5H18.11
10	80	8.8	795	2	F82858	dipeptidyl-peptida
11	79.5	8.7	548	2	D90493	hypothetical prote
12	78	8.6	450	2	A45547	tubulin alpha-II c
13	78	8.6	1128	2	H90538	hypothetical prote
14	77.5	8.5	338	2	T23520	hypothetical prote
15	77.5	8.5	858	1	A42239	adenylate cyclase
16	77	8.4	828	2	G87584	hypothetical prote
17	76	8.3	391	2	T36311	probable lipase -
18	76	8.3	422	2	E69892	endo-xyylanase homo
19	76	8.3	450	2	S31399	tubulin alpha chai
20	76	8.3	451	2	S04694	tubulin alpha chai
21	76	8.3	502	2	H81273	probable amino aci
22	76	8.3	603	2	T16298	hypothetical prote
23	75.5	8.3	162	2	D69439	conserved hypothet
24	75.5	8.3	989	2	I56333	apolipoprotein B -
25	75.5	8.3	1138	2	G71554	probable transmemb
26	75	8.2	275	2	B98301	non-heme chloroper
27	75	8.2	275	2	AF2982	non-heme chloroper
28	75	8.2	453	2	S16339	tubulin alpha chai
29	74.5	8.2	292	2	T33987	hypothetical prote

A;Experimental source: liver
C;Comment: This enzyme converts platelet-activating factor to an inactive metabolite lys
C;Keywords: glycoprotein; hydrolase
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-436/Product: platelet-activating factor-acetylhydrolase #status predicted <WAT>
F;76,200,324/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 68.8%; Score 627.5; DB 2; Length 436;
Best Local Similarity 70.8%; Pred. No. 3.9e-53;
Matches 121; Conservative 19; Mismatches 26; Indels 5; Gaps 1;

QY 1 GHSFGGATVIQTLSQDQFRGCIADAWMPPLGDEVYSRIPOPLFFINSEYFQYPAIIK 60
DB 269 GHSFGGATVIQTLSQDQFRGCIADAWMPPLGDEVYSRIPOPLFFINSEYFQYPAIIK 328
QY 61 MKKCYSPDKERKMTITRGSVHQNFAFTFATGKIIGHMLKLGIDISNAIDLSNKASLA 120
DB 329 IEKPYQOKERKMTAVKSVHNFVDFATGKIIGHMLKLGIDISNAIDLSNKASLA 389
QY 121 FLQHLGLHDKFDQDCLIEGDDNLTGNTNTOHMLQNSGGIEKYN 171
DB 389 FLQYLGDKNFQDQNSLMEGDDNLTPEFTIPTT-----MQSSTGTGEQRN 434

RESULT 3
T32756
hypothetical protein W03G9.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T32756
R;Dante, M.; Keppler, D.
submitted to the EMBL Data Library, December 1997
A;Description: The sequence of C. elegans cosmid W03G9.
A;Reference number: Z21220
A;Accession: T32756
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-384 <DN>
A;Cross-references: UNIPROT:O44753; EMBL:AF039716; PIDN:AA96738.1; GSPDB:GN00019; CESP:
A;Experimental source: strain Bristol N2; clone W03G9
C;Genetics:
A;Gene: CESP:W03G9.6
A;Map position: 1
A;Introns: 47/3; 90/2; 142/2; 183/3; 333/3

Query Match 20.4%; Score 186; DB 2; Length 384;
Best Local Similarity 32.5%; Pred. No. 2.7e-10;
Matches 40; Conservative 26; Mismatches 55; Indels 2; Gaps 1;

QY 1 GHSFGGATVIQTLSQDQFRGCIADAWMPPLGDEVYSRIPOPLFFINSEYFQYPAIIK 60
DB 234 GHSFGGATSIASSSD--FQKAIYLDGMYPLDQNOQEQAKQPTIMFLNVGDQWQNNLEV 291
QY 61 MKKCYSPDKERKMTITRGSVHQNFAFTFATGKIIGHMLKLGIDISNAIDLSNKASLA 120
DB 292 MRKILPNEGNIILTLGAVHQSFDTDPFPFVFNWAKQFGVGHGTEPYLCMQSAIETLS 351

QY 121 FLQ 123
DB 352 FLK 354

RESULT 4
T28936
hypothetical protein C52B9.7 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 18-Feb-2000
C;Accession: T28936
R;Neison, J.
submitted to the EMBL Data Library, July 1996
A;Description: The sequence of C. elegans cosmid C52B9.
A;Reference number: Z20545
A;Accession: T28936

A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-476 <NEL>
A;Cross-references: EMBL:U64598; PIDN:AAC47973.1; GSPDB:GN00028; CESP:C52B9.7
A;Experimental source: strain Bristol N2; clone C52B9
C;Genetics:
A;Gene: CESP:C52B9.7
A;Map position: X
A;Introns: 23/3; 70/2; 121/3; 164/2; 273/3; 343/3; 425/3

Query Match 20.2%; Score 184; DB 2; Length 476;
Best Local Similarity 32.5%; Pred. No. 5.6e-10;
Matches 40; Conservative 24; Mismatches 59; Indels 0; Gaps 0;

QY 1 GHSFGGATVIQTLSQDQFRGCIADAWMPPLGDEVYSRIPOPLFFINSEYFQYPAIIK 60
DB 324 GHSFGGATSIASSAYTTDFQKAIYFDGMYPLDSTQEQAKQPTIMFLNVGDQWQNNLEV 383
QY 61 MKKCYSPDKERKMTITRGSVHQNFAFTFATGKIIGHMLKLGIDISNAIDLSNKASLA 120
DB 384 MKKIISHNDGNLALTNGAVHQCFSDFPFIPFSLAKKFGVGRTEPSLCMQAAIELSLA 443

QY 121 FLQ 123
DB 444 FLE 446

RESULT 5
T39268
hypothetical protein SPBC106.11c - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T39268
R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Davis, P.; Churcher, C.M.
submitted to the EMBL Data Library, August 1999
A;Reference number: Z21840
A;Accession: T39268
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-438 <LVN>
A;Cross-references: UNIPROT:Q9URV1; EMBL:AL110295; PIDN:CAB53727.1; GSPDB:GN00067; SPDB:
A;Experimental source: strain 972h; cosmid c106
C;Genetics:
A;Gene: SPDB:SPBC106.11c
A;Map position: 2

Query Match 14.6%; Score 133; DB 2; Length 438;
Best Local Similarity 23.4%; Pred. No. 4.6e-05;
Matches 44; Conservative 39; Mismatches 57; Indels 48; Gaps 8;

QY 1 GHSFGGATV-----IQTLSQDQFRGCIADAWMPPLGDEVYSRIPOPLFFIN 48
DB 255 GHSFGGAATCAFTSGSSTKSLYNDYMFHTEFKCSILYDINWLPVROLHLSTMYRPTLMII 314
QY 49 SEYFQYPAIIKMKCY-----SPDKERKMTITR-----GSHVQNFADF 87
DB 315 YEFRRVDNFQALSVLWKNKDSQNSAGSDEKMSVPLKYSVHVVDYDGTVHANSQDL 374

QY 88 TFATGKIIGHMLKLGIDISNAIDLSNKASLAFLQHLGLHDKFDQDCLIEGDDN 144
DB 375 PILLPRVLRVLKGFADPYEALINTRSSVQFLREN---HVE-----NVQGDNDPSS 425

QY 145 ---NLIPG 149
DB 426 LQTNIIIPG 433

RESULT 6
G83740
hypothetical protein BH0727 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C;Accession: G83740

R; Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A; Title: Complete genome sequence of the alkaliphilic bacterium *Bacillus halodurans* and
A; Reference number: A83650; MUID:20512582; PMID:11058132
A; Accession: G83740
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-450 <STO>
A; Cross-references: UNIPROT:Q9KEX2; GB:AP001509; GB:BA000004; NID:G10173176; PIDN:BA0044
A; Experimental source: strain C-125
C; Genetics:
A; Gene: BH0727

```

Query Match      14.2%; Score 129.5; DB 2; Length 450;
Best Local Similarity 23.5%; Pred. No. 0.0001;
Matches 35; Conservative 28; Mismatches 49; Indels 37; Gaps 5;

Qy 1 GHSFGGATVQTLSEDFRCGIALDAMWPLGDEVYSRIPQPIFFINS----- 49
      |||||
Db 315 GHSFGGATTAVQVHQDPRIIRAGVNMGDGFLP--GSLIEGLDYPFMYSGVEEVSMEGPDG 372
      |||||

Qy 50 ---EYFOYPAIIKKWKCYSPDKERK-----MITIRGSVHNTADFTFATGKIIGH 97
      |||||

Db 373 KYVEEARLPE---EFREFIADDKRKKEGALKKNGLYVVIENAEHESFDWMLYSPLLDR 429
      |||||

Qy 98 MLKLKGDIDSNAADLSNKASLAFLOKHL 126
      :|||

Db 430 DLPW-----LDOINKTLLDFDEHLL 449
      :|||

```

RESULT 7
D64220
methyltransferase ssoIM homolog - Mycoplasma genitalium
C:Species: Mycoplasma genitalium
C:Date: 17-Nov-1995 #sequence_revision 17-Nov-1995 #text_change 09-Jul-2004
C:Accession: D64220
R.;Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.;
M.; Fuhrmann, J.; Nguyen, D.; Utterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, J.
C.A.; Venter, J.C.
Science 270, 397-403, 1995
A:Title: The minimal gene complement of Mycoplasma genitalium.
A:Reference number: A64200; MUID:96046346; PMID:7569993
A:Accession: D64220
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-317 <TIGR>
A:Cross-references: UNIPROT:Q49400; GB:U39695; GB:L43967; NID:gi045833; PID:gi045869; TT:
A:Experimental source: strain G-37
C:Genetics:
A:Genetic code: SGC3
A:Start codon: GTG
C:Superfamily: site-specific methyltransferase EcoRI

Query Match	9.2%;	Score 84;	DB 2;	Length 317;
Best Local Similarity	25.4%;	Pred. No. 1.8;		
Matches	30;	Conservative	20; Mismatches	48; Indels
Gaps	4;			

Qy	48	NSEYFQY---	PANIIMKKVCSPDKERKMII	TIRGSVHQNFAD---	FTFATCKIIGHMLKL	101
		:	:: :	:	: :	
	47	NSHFFQFPQTNFNQLK--	-----LIGFSNNLSQADKFTFDG	NKVTKTLKG	94	
Db						
Qy	102	KGDIIDSNAIDL	SNKSAFLQKLGLHKPDPQWDCLIEGDENLI	POTNINTNTNQHI	159	
		:	:::	:	:	
Db	95	NGDFSSDESIEVLKQADITVTNP	PFPSIQSF--IDLLTIQHKNQFLVJLGNAASVYNHI	150		
		:	:::	:	:	

```

RESULT 8
S56151
tubulin alpha chain - Spathidium sp. (fragment)
C:Species: Spathidium sp.
C:Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 09-Jul-2004
C:Accession: S56151
R:Tourancheau, A.B.: Tsao, N.; Klobutcher, L.A.; Pearlman, R.E.; Adoutte, A.

```

EMBO J. 14, 3262-3267, 1995
A>Title: Genetic code deviations in the ciliates: evidence for multiple and independent
A:Reference number: S56148; MUID:95347352; PMID:7621837
A:Accession: S56151
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-382 <TOU>
A:Cross-references: UNIPROT:Q27216; EMBL:Z49848; NID:g861141; PID:g8611
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1995
C:Superfamily: tubulin
C:Keywords: heterodimer; microtubule

	Query Match	9.1%	Score 83;	DB 2;	Length 382;
	Best Local Similarity	22.6%;	Pred. No. 2.8;		
	Matches	40;	Conservative	29;	Mismatches 68;
					Indels 40;
					Gaps 9
Qy	7	ATVQTISEDORFRCGIALDAMWPLGDEVYSRIPQLFFINSEYFQYPAIIKMKKCVS	66		
Db	202	AQVISSLTASLRFQGANVDVTFQTNLVPFRI-----HFWLSSY----APIISAEKAY-	252		
Qy	67	PKERKMITITGSVHQNADFPTFAT-----GKIIGHMLKLKGDI-----DSNAAI--DLSNKK	116		
Db	253	-----HEQLSVAEITNSSFEFASMAWXCDPRHGKYMACCMYRGDVPKDVNAVAATIKTK	308		
Qy	117	ASLAFLOKHLGLHKDFQW-----DCUIEGDDENLIPGTNINTTNNQHI--MLQNSSGI	167		
Db	309	RTI-----OFDWCPTGPKCGINYPPTVPFGGDLAKVMRYACMISNSTAI	354		

RESULT 9
A86318
protein F15H18.11 [imported] - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C/Accession: A86318
R/Chnologists: A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
C.; C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A/Authors: Hunter, J.B.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A/Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A/Reference number: A86141; MUID:21016719; PMID:11130712
A/Accession: A86318
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-1154 <STO>
A/Cross-references: UNIPROT:Q9LPQ6; GB:AE005172; NID:g6714300; PIDN:AAF25996.1; GSPDB:GN
C/Genetics:
A/Gene: F15H18.11
A/Map position: 1

	Query Match	9.0%;	Score 82.5;	DB 2;	Length 1154;
	Best local Similarity	26.3%;	Pred. No. 13;		
	Matches	36;	Conservative 22;	Mismatches 60;	Indels 19; Gaps 6;
Qy	45	FFINSEYFQYPANIIKMKKCYSPDKERKMITIR----	GSVHQFADFT-----	FATGKI	94
Db	6	FFISFVVF-----	SVADLPSCFSDAQOYEECRSRNLTCGSGHRVFESTTYPFWGGFNPKPF	61	
Qy	95	IGH-MLKGLKDIDSNRAAIDLSNKSASLAFLOKHGLGHLKDFDQWCLIEGGDDENILPGTNIN	153		
Db	62	CGHSSFKLSCGEQNLTLAGN-ITLFRVVSANLEHDHKISVADDSLLDDGGCLNI----	WNFN	117	
Qy	154	TTNQHIMLNSSGIEKY	170		
Db	118	GKNOFTLDSNTETIDVF	134		

RESULT 10

Query Match	8.7%	Score 79.5;	DB 2;	Length 548;
Best Local Similarity	26.2%;	Pred. No. 9.6;		
Matches 27;	Conservative	23;	Mismatches 34;	Indels 19;
				Gaps 6;

Db 155 DTIVSQPEILFNINSQ----PSSNVPLNKSIRNISEEDFLAPKAQFGEKYNIKIVNRDI

Query Match	8.7%	Score 79.5;	DB 2;	Length 548;
Best Local Similarity	26.2%;	Pred. No. 9.6;		
Matches 27;	Conservative	23;	Mismatches 34;	Indels 19;
				Gaps 6;

Qy 70 ERKMITIRGSHVQNFADFTATGKIIGHMLKLGKGDIDSNAIDLSNKASLAFLOKHLGLH 129
Db 211 EKNILITLIEISVRDETSSNEQTNTYSGYTKVISNLTDHLSVSLNHFQOESSQIRLGFR 270
Qy 130 KDFQDQWCLIEGDDENLIPGTNINTTNOHIMLQNSSGIE 168
Db 271 KNSS--DNLEQRADENILP--SLUKENFGLQSEGQIE 305

RESULT 14

T23520
hypothetical protein K08H2.8 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T23520
R:Gajadety, S.
submitted to the EMBL Data Library, March 1996
A:Reference number: Z19751
A:Accession: T23520
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-338 <WIL>
A:Cross-references: UNIPROT:Q21372; EMBL:Z70210; PIDN:CAA94154.1; GSPDB:GN00028; CESP:K08H2
A:Experimental source: clone K08H2
C:Genetics:
A:Gene: CESP:K08H2.8
A:Map position: X
A:Introns: 9/3; 31/1; 80/1; 131/3; 157/3; 185/3; 216/2; 305/3

Query Match 8.5%; Score 77.5; DB 2; Length 338;
Best Local Similarity 22.8%; Pred. No. 8.2; Mismatches 52; Indels 19; Gaps 4;
Matches 28; Conservative 24

Qy 60 KMKKCYSPDKERKMI-----TIRGSHVQNFADFTATGKI-IGHMLKLGKGDIDSNA-- 110
Db 89 RLAKCYAVGMDKAVQPKREVHTSNGSFQDQNDPDYDLRLGGTRTSPSVLSSDMTSPGSA 148
Qy 111 -----IDLSNKASLAFLOKHLGLHKLDFDQW-----DCLIEGDDENLIPGTNINTTNOHIM 160
Db 149 FTPLNINLATLLRAFALKYMLLDNVYHTVELGPRDLVLVNNNYIVPGVPINFKGSDVV 208
Qy 161 LQN 163
Db 209 DEN 211

RESULT 15

A42239
adenylate cyclase (EC 4.6.1.1) germination stage - slime mold (Dictyostelium discoideum)
C:Species: Dictyostelium discoideum
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A42239
R:Pitt, G.S.; Milona, N.; Borleis, J.; Lin, K.C.; Reed, R.R.; Devreotes, P.N.
Cell 69, 305-315, 1992
A:Title: Structurally distinct and stage-specific adenylyl cyclase genes play different
A:Reference number: A42239; MUID:92233467; PMID:1348970
A:Accession: A42239
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A:Molecule type: DNA
A:Residues: 1-858 <PIT>
A:Cross-references: GB:M87278
C:Superfamily: slime mold germination stage adenylyl cyclase; guanylate cyclase catalyt
C:Keywords: phosphorus-oxygen lyase
F:351-574/Domain: guanylate cyclase catalytic domain homology <GCC>

Query Match 8.5%; Score 77.5; DB 1; Length 858;
Best Local Similarity 21.2%; Pred. No. 27;
Matches 36; Conservative 24; Mismatches 75; Indels 35; Gaps 6;

Qy 36 VYSRIPQPLFFINSEY-----FQYPANIIKMKCYSPDKERKMITIRG-----S 79
Db 604 IYPEFPGCLQALNIENNLTNDAGCENCSKILKTYAYSPDHSYNYHHGDDNSPPPPS 663

Qy 80 VHQN-----PADFTATGKIIGH-----MLKLGKGDIDSNAIDLSN-----KASLAFLOK 124
Db 664 LNSNDLIDGSEYHDDPPPSDSNVGYHDTSKDIKEDENEQNETLLFNOEQLKKKQIENIQ 723
Qy 125 HLGHLKDFDQWCLIEGDDENL-----IPGTNINTTNOHIMLQNSSGIEKY 170
Db 724 DLSLDSIEAIKILNNNNNNNNNDNNINNTLNNNNNNDINNNSDNVNYY 773

Search completed: March 15, 2005, 10:08:37
Job time : 15.25 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 15, 2005, 09:48:35 ; Search time 63.7059 Seconds
(without alignments)
1374.528 Million cell updates/sec

Title: US-09-922-067F-14_COPY_271_441

Perfect score: 912

Sequence: 1 GHSFGGATVIQTLSEQDQFR.....INTTNQHMLQNSSGIEKYN 171

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	908	99.6	441	1 PAPA_HUMAN	Q13093 h platelet-
2	776	85.1	444	1 PAPA_BOVIN	Q28017 b platelet-
3	749	82.1	444	1 PAPA_CANFA	Q28262 c platelet-
4	634	69.5	440	2 Q921T4	Q921T4 mus musculus
5	633	69.4	440	2 Q8BKM3	Q8BKM3 mus musculus
6	627.5	68.8	436	1 PAPA_CAVPO	P70683 c platelet-
7	592	64.9	440	1 PAPA_MOUSE	Q60963 m platelet-
8	537.5	58.9	422	1 PAPA_CHICK	Q90678 g platelet-
9	535	58.7	404	2 Q6NYI7	Q6NY17 brachydanio
10	355	38.9	392	1 PAF2_HUMAN	P83006 rattus norv
11	350	38.4	390	1 PAF2_RAT	Q99487 homo sapien
12	338	37.1	390	1 PAF2_MOUSE	Q8Vdg7 mus musculus
13	335	36.7	392	1 PAF2_BOVIN	P79106 bos taurus
14	308	33.8	362	2 Q6GPX8	Q6GPX8 xenopus lae
15	304	33.3	346	2 Q9DB74	Q9DB74 mus musculus
16	186	20.4	384	2 Q44753	Q44753 caenorhabdi
17	184	20.2	388	1 PAPA_CAEBL	Q22943 caenorhabdi
18	139	15.2	920	2 Q7SCR4	Q7SCR4 neorospira
19	133	14.6	438	2 Q9URV1	Q9URV1 schizosacch
20	129.5	14.2	450	2 Q9KEX2	Q9KEX2 bacillus ha
21	105.5	11.6	609	2 Q7S2B3	Q7S2B3 neorospira
22	104	11.4	468	2 Q81UC8	Q81UC8 bacillus th
23	104	11.4	468	2 Q6HML0	Q6HML0 bacillus th
24	102.5	11.2	402	2 Q70K06	Q70K06 bacillus am
25	97	10.6	378	2 Q651Y4	Q651Y4 bacillus li
26	97	10.6	468	2 Q73CM7	Q73CM7 bacillus ce
27	96	10.5	468	2 Q81H53	Q81H53 bacillus ce
28	94.5	10.4	386	2 Q9F2X9	Q9F2X9 streptomyce
29	92.5	10.1	509	2 Q8LSC7	Q8LSC7 brassica ca
30	90	9.9	456	2 Q81EZ5	Q81EZ5 bacillus ce
31	89.5	9.8	3589	2 Q61F63	Q61F63 plasmodium

32 88 9.6 331 2 Q7NJZ2
33 86.5 9.5 509 2 Q8S384
34 85.5 9.4 504 2 Q2M36
35 84.5 9.3 699 2 Q8MS38
36 84.5 9.3 801 2 Q8EHB8
37 84 9.2 317 1 Y184 MYCGE
38 83.5 9.2 1458 2 Q8QTB8
39 83.5 9.2 2330 2 Q91L86
40 83.5 9.2 4180 2 Q8VAQ8
41 83 9.1 382 2 Q27216
42 82.5 9.0 249 2 Q8RX30
43 82.5 9.0 401 2 Q82QK6
44 82.5 9.0 1154 2 Q9LPQ6
45 81.5 8.9 543 2 Q8PX46

Q7njz2 gloeobacter
Q8s384 brassica ju
Q2m36 rhizobium m
Q8ms38 drosophila
Q8ehb8 shewanella
Q49400 mycoplasma
Q8qtb8 white spot
Q91l86 white spot
Q8vaq8 white spot
Q27216 spathidium
Q8rx30 arabidopsis
Q82qn6 streptomyce
Q9lpq6 arabidopsis
Q8px46 methanosaarc

ALIGNMENTS

RESULT 1

PAPA_HUMAN
ID PAPA_HUMAN STANDARD; PRT; 441 AA.
AC Q13093; Q15692; Q81VA2;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Platelet-activating factor acetylhydrolase precursor (EC 3.1.1.47)
DE (PAF acetylhydrolase) (PAF 2-acetylhydrolase) (LDL-associated
DE phospholipase A2) (LDL-PLA(2)) (2-acetyl-1-alkylglycerophosphocholine
DE esterase) (1-alkyl-2-acetyl-1-alkylglycerophosphocholine esterase).
GN Name=PLA2G7; Synonyms=PAPAH;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 42-57.
RC TISSUE=Myeloid;
RX MEDLINE=95214779; PubMed=7700381; DOI=10.1038/374549a0;
RA Tjoelker L.W., Wilder C., Eberhardt C., Stafforini D.M., Dietsch G.,
RA Schimpf B., Hooper S., le Trong H., Couzens L.S., Zimmerman G.A.,
RA Yanada Y., McIntyre T.M., Prescott S.M., Gray P.W.;
RA "Anti-inflammatory properties of a platelet-activating factor
RT acetylhydrolase.";
RL Nature 374:549-553 (1995).
RN [2]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Lymphoma;
RX MEDLINE=96197208; PubMed=8624782;
RA Tew D.G., Southan C., Rice S.Q.J., Lawrence M.P., Li H., Boyd H.F.,
RA Moores K., Gloger I.S., Macphie C.H.;
RA "Purification, properties, sequencing, and cloning of a lipoprotein-
RT associated, serine-dependent phospholipase involved in the oxidative
RT modification of low-density lipoproteins.";
RL Arterioscler. Thromb. Vasc. Biol. 16:591-599 (1996).
RN [3]
RP SEQUENCE FROM N.A., AND VARIANT ALA-379.
RC TISSUE=Blood;
RX MEDLINE=12477932; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Straube R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Kryzinski M.I., Skalska U., Zimmerman G.A.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.",
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP MUTAGENESIS.
RX MEDLINE=96029630; PubMed=7592717; DOI=10.1074/jbc.270.43.25481;
RA Tjoelker L.W., Eberhardt C., Unger J., le Trong H., Zimmerman G.A.,
RA McIntyre T.M., Stafforini D.M., Prescott S.M., Gray P.W.,
RT "Plasma platelet-activating factor acetylhydrolase is a secreted
RT phospholipase A2 with a catalytic triad.",
RL J. Biol. Chem. 270:25481-25487(1995).
RN [5]
RP VARIANT PLA2G7 DEFICIENCY PHE-279.
RX MEDLINE=96259525; PubMed=8675689.
RA Stafforini D.M., Satoh K., Atkinson D.L., Tjoelker L.W., Eberhardt C.,
RA Yoshida H., Imaizumi T., Takamatsu S., Zimmerman G.A., McIntyre T.M.,
RA Gray P.W., Prescott S.M.,
RT "Platelet-activating factor acetylhydrolase deficiency. A missense
RT mutation near the active site of an anti-inflammatory phospholipase.",
RL J. Clin. Invest. 97:2784-2791(1996).
RN [6]
RP VARIANT PLA2G7 DEFICIENCY ARG-281.
RX MEDLINE=97396177; PubMed=9245731; DOI=10.1006/bbr.1997.7047;
RA Yamada Y., Yokota M.,
RA "Loss of activity of plasma platelet-activating factor acetylhydrolase
RA due to a novel Gln281-->Arg mutation.",
RL Biochem. Biophys. Res. Commun. 236:772-775(1997).
RN [7]
RP VARIANT PLA2G7 DEFICIENCY PHE-279.
RX MEDLINE=98074100; PubMed=9412624;
RA Hiramoto M., Yoshida H., Imaizumi T., Yoshimizu N., Satoh K.,
RA "A mutation in plasma platelet-activating factor acetylhydrolase
RA (Val279-->Phe) is a genetic risk factor for stroke.",
RL Stroke 28:2417-2420(1997).
RN [8]
RP VARIANT PLA2G7 DEFICIENCY PHE-279.
RX MEDLINE=98132308; PubMed=9472966;
RA Yamada Y., Ichihara S., Fujimura T., Yokota M.,
RA "Identification of the G94-->T missense in exon 9 of the plasma
RA platelet-activating factor acetylhydrolase gene as an independent risk
RA factor for coronary artery disease in Japanese men.",
RL Metabolism 47:177-181(1998).
RN [9]
RP VARIANT PLA2G7 DEFICIENCY PHE-279.
RX MEDLINE=98430412; PubMed=9759612;
RA Yoshida H., Imaizumi T., Fujimoto K., Itaya H., Hiramoto M.,
RA Yoshimizu N., Fukushi K., Satoh K.,
RA "A mutation in plasma platelet-activating factor acetylhydrolase
RA (Val279Phe) is a genetic risk factor for cerebral hemorrhage but not
RA for hypertension.",
RL Thromb. Haemost. 80:372-375(1998).
RN [10]
RP VARIANTS HIS-92; THR-198 AND ALA-379.
RX MEDLINE=20311534; PubMed=10733466;
RA Kruse S., Mao X.-Q., Heinzmann A., Blattmann S., Roberts M.H.,
RA Braun S., Gao P.-S., Forster J., Kuehr J., Hopkin J.M., Shirakawa T.,
RA Deichmann K.A.,
RA "The Ile198Thr and Ala379Val variants of plasmatic PAF-acetylhydrolase
RA impair catalytic activities and are associated with atopy and
RA asthma.",
RL Am. J. Hum. Genet. 66:1522-1530(2000).
CC -1- FUNCTION: Modulates the action of platelet-activating factor (PAF)
CC by hydrolyzing the sn-2 ester bond to yield the biologically
CC inactive lyso-PAF. Has a specificity for substrates with a short
CC residue at the sn-2 position. It is inactive against long-chain
CC phospholipids.
CC -1- CATALYTIC ACTIVITY: 1-alkyl-2-acetyl-sn-glycero-3-phosphocholine +
CC H(2)O = 1-alkyl-sn-glycero-3-phosphocholine + acetate.
CC -1- SUBCELLULAR LOCATION: Extracellular.
CC -1- TISSUE SPECIFICITY: Plasma.

CC -1- POLYMORPHISM: The alleles Thr-198 and Val-379 are associated with
CC atopy and asthma.
CC -1- DISEASE: Defects in PLA2G7 are the cause of platelet-activating
CC factor acetylhydrolase deficiency (PLA2G7 deficiency)
CC [MIM:601690]. It is a trait which is present in 27% of Japanese.
CC It could have a significant physiologic effect in the presence of
CC inflammatory bodily responses.
CC -1- SIMILARITY: Belongs to the AB hydrolase superfamily. Lipase
CC family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U20157; AAC50126.1; -.
CC EMBL; U24577; AAB04170.1; -.
CC EMBL; BC038452; AAB38452.1; -.
CC PIR; S60247; S60247.
CC Gene; HGNC:9040; PLA2G7.
CC MIM; 601690; -.
CC GO; GO:0005576; C:extracellular; TAS.
CC GO; GO:0005543; F:phospholipid binding; TAS.
CC GO; GO:0006954; P:inflammatory response; TAS.
CC GO; GO:0006629; P:lipid metabolism; TAS.
CC InterPro; IPR008262; Lipase_AS.
CC InterPro; IPR005065; PAF_Ac_hydrol_II.
CC InterPro; IPR000379; Ser_estrs.
CC Pfam; PFO3403; PAF-AH_P_II; 1.
CC Direct protein sequencing; Disease mutation; Glycoprotein; Hydrolase;
CC Lipid degradation; Polymorphism; Signal.
CC SIGNAL 1 21
CC CHAIN 22 441 Platelet-activating factor
CC ACT_SITE 273 273 acetylhydrolase.
CC ACT_SITE 296 296 Charge relay system.
CC ACT_SITE 351 351 Charge relay system.
CC CARBOHYD 423 423 N-linked (GlcNAc...) (Potential).
CC CARBOHYD 433 433 N-linked (GlcNAc...)
CC VARIANT 92 92 R -> H (common polymorphism;
CC dbSNP:1805017).
CC VARIANT 198 198 dbSNP:1805017.
CC VARIANT 279 279 I -> T (common polymorphism;
CC dbSNP:1805018).
CC VARIANT 279 279 V -> F (in PLA2G7 deficiency; loss of
CC function; more common among Japanese than
CC in Caucasians; risk factor for coronary
CC artery disease and stroke).
CC VARIANT 281 281 /FTid=VAR_004268.
CC VARIANT 281 281 Q -> R (in PLA2G7 deficiency; loss of
CC function).
CC VARIANT 379 379 V -> A (common polymorphism;
CC dbSNP:1051931).
CC VARIANT 379 379 /FTid=VAR_011585.
CC MUTAGEN 108 108 S->A: Activity is higher than wild type.
CC MUTAGEN 273 273 S->A: Loss of activity.
CC MUTAGEN 286 286 D->A: Almost no activity.
CC MUTAGEN 286 286 D->N: Diminished activity.
CC MUTAGEN 296 296 D->A: Loss of activity.
CC MUTAGEN 296 296 D->N: Loss of activity.
CC MUTAGEN 304 304 D->A: No change in activity.
CC MUTAGEN 338 338 D->A: Activity is higher than wild type.
CC MUTAGEN 351 351 H->A: Loss of activity.
CC SEQUENCE 441 AA; 50077 MW; 3BA9EAE8094A57 CRC64;
CC
CC Query Match 99.6%; Score 908; DB 1; Length 441;
CC Best Local Similarity 99.4%; Pred. No. 1.7e-79;

Matches 170; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GHSFGGATVIQTLSEDOFRFGIADAWMPPLGDEVYSRIPQPLFFINSEYFOYPANIIK 60
 |||||
 DB 271 GHSFGGATVIQTLSEDOFRFGIADAWMPPLGDEVYSRIPQPLFFINSEYFOYPANIIK 330
 |||||

QY 61 MKKCYSPDKERKMITIRGSHVQNFADFTFATGKIIGHMLKLGKIDISNAIDLNSKASLA 120
 |||||
 DB 331 MKKCYSPDKERKMITIRGSHVQNFADFTFATGKIIGHMLKLGKIDISNAIDLNSKASLA 390
 |||||

QY 121 FLOKHGLGKDFQDWDCLIEGDENLIPGTNTNTNOHIMLQNSSGIEKYN 171
 |||||
 DB 391 FLOKHGLGKDFQDWDCLIEGDENLIPGTNTNTNOHIMLQNSSGIEKYN 441
 |||||

RESULT 2

PAFA_BOVIN

ID PAFA_BOVIN STANDARD; PRT; 444 AA.

AC Q28017;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE Platelet-activating factor acetylhydrolase precursor (EC 3.1.1.47)

DE (PAF acetylhydrolase) (PAF 2-acylhydrolase) (LDL-associated

DE phospholipase A2) (LDL-PLA(2)) (2-acetyl-1-alkylglycerophosphocholine

DE esterase) (1-alkyl-2-acetyl-glycerophosphocholine esterase).

DE Name=PLA2G7;

GN Bos taurus (Bovine).

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Bovinae; Bos.

OX NCBI_TaxID=9913;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Spleen;

RX MEDLINE=96029630; PubMed=7592717; DOI=10.1074/jbc.270.43.25481;

RA Tjoelker L.W., Eberhardt C., Unger J., Trong H.L., Zimmerman G.A.,

RA McIntyre T.M., Stafforini D.M., Prescott S.M., Gray P.W.;

RT "Plasma platelet-activating factor acetylhydrolase is a secreted

RT phospholipase A2 with a catalytic triad.;"

RL J. Biol. Chem. 270:25481-25487(1995).

CC -1- FUNCTION: Modulates the action of platelet-activating factor (PAF)

CC by hydrolyzing the sn-2 ester bond to yield the biologically

CC inactive lyso-PAF. Has a specificity for substrates with a short

CC residue at the sn-2 position. It is inactive against long-chain

CC phospholipids.

CC -1- CATALYTIC ACTIVITY: 1-alkyl-2-acetyl-sn-glycero-3-phosphocholine +

CC H2O = 1-alkyl-sn-glycero-3-phosphocholine + acetate.

CC -1- SUBCELLULAR LOCATION: Extracellular.

CC -1- TISSUE SPECIFICITY: Plasma.

CC -1- SIMILARITY: Belongs to the AB hydrolase superfamily. Lipase

CC family.

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CC -----

EMBL; U34247; AAC48483.1; --

DR InterPro; IPR008262; Lipase_AS.

DR InterPro; IPR005065; PAF_Ac_hydrolp_II.

DR InterPro; IPR003379; Ser_estra.

DR Pfam; PF03403; PAF-AH_P_II; 1.

DR PROSITE; PS00120; LIPASE_SER; 1.

KW Glycoprotein; Hydrolase; Lipid degradation; Signal.

FT SIGNAL 1 21 By similarity.

FT CHAIN 22 444 Platelet-activating factor

FT acetylhydrolase.

FT ACT_SITE 274 274 Charge relay system (By similarity).

FT FT 297 Charge relay system (By similarity).

FT ACT_SITE 352 352 Charge relay system (By similarity).

FT CARBOHYD 60 N-linked (GlcNAc...) (potential).

FT CARBOHYD 200 200 N-linked (GlcNAc...) (potential).

FT CARBOHYD 424 424 N-linked (GlcNAc...) (potential).

FT CARBOHYD 434 434 N-linked (GlcNAc...) (potential).

SQ SEQUENCE 444 AA; 50133 MW; 97689917BE2F4C38 CRC64;

Query Match 85.1%; Score 776; DB 1; Length 444;

Best Local Similarity 84.2%; Pred. No. 1.1e-66;

Matches 144; Conservative 12; Mismatches 15; Indels 0; Gaps 0;

QY 1 GHSFGGATVIQTLSEDOFRFGIADAWMPPLGDEVYSRIPQPLFFINSEYFOYPANIIK 60
 |||||
 DB 272 GHSFGGATVIQTLSEDOFRFGIADAWMPPLGDEVYSRIPQPLFFINSEYFOYPANIIK 331
 |||||

QY 61 MKKCYSPDKERKMITIRGSHVQNFADFTFATGKIIGHMLKLGKIDISNAIDLNSKASLA 120
 |||||
 DB 332 MKKCYSPDKERKMITIRGSHVQNFADFTFATGKIIGHMLKLGKIDISNAIDLNSKASLA 391
 |||||

QY 121 FLOKHGLGKDFQDWDCLIEGDENLIPGTNTNTNOHIMLQNSSGIEKYN 171
 |||||
 DB 392 FLOKHGLGKDFQDWDCLIEGDENLIPGTNTNTNOHIMLQNSSGIEKYN 442
 |||||

RESULT 3

PAFA_CANFA

ID PAFA_CANFA STANDARD; PRT; 444 AA.

AC Q28252;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE Platelet-activating factor acetylhydrolase precursor (EC 3.1.1.47)

DE (PAF acetylhydrolase) (PAF 2-acylhydrolase) (LDL-associated

DE phospholipase A2) (LDL-PLA(2)) (2-acetyl-1-alkylglycerophosphocholine

DE esterase) (1-alkyl-2-acetyl-glycerophosphocholine esterase).

GN Name=PLA2G7;

OS Canis familiaris (Dog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

OX NCBI_TaxID=9615;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Spleen;

RX MEDLINE=96029630; PubMed=7592717; DOI=10.1074/jbc.270.43.25481;

RA Tjoelker L.W., Eberhardt C., Unger J., Trong H.L., Zimmerman G.A.,

RA McIntyre T.M., Stafforini D.M., Prescott S.M., Gray P.W.;

RT "Plasma platelet-activating factor acetylhydrolase is a secreted

RT phospholipase A2 with a catalytic triad.;"

RL J. Biol. Chem. 270:25481-25487(1995).

CC -1- FUNCTION: Modulates the action of platelet-activating factor (PAF)

CC by hydrolyzing the sn-2 ester bond to yield the biologically

CC inactive lyso-PAF. Has a specificity for substrates with a short

CC residue at the sn-2 position. It is inactive against long-chain

CC phospholipids.

CC -1- CATALYTIC ACTIVITY: 1-alkyl-2-acetyl-sn-glycero-3-phosphocholine +

CC H2O = 1-alkyl-sn-glycero-3-phosphocholine + acetate.

CC -1- SUBCELLULAR LOCATION: Extracellular.

CC -1- TISSUE SPECIFICITY: Plasma.

CC -1- SIMILARITY: Belongs to the AB hydrolase superfamily. Lipase

CC family.

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CC -----

EMBL; U34246; AAC48484.1; --

DR InterPro; IPR008262; Lipase_AS.

DR InterPro; IPR005065; PAF_Ac_hydrolp_II.

DR InterPro; IPR003379; Ser_estra.


```

RL  Genome Res. 10:1617-1630 (2000).
RN  [5]
RP  SEQUENCE FROM N.A.
RC  STRAIN=C57BL/6J; TISSUE=Spinal ganglion;
RX  MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA  Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
RA  Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA  Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA  Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA  Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA  Onoda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA  Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.,
RT  "RIKEN integrated sequence analysis (RISA) system-384-format
RT  sequencing pipeline with 384 multicapillary sequencer.";
RL  Genome Res. 10:1757-1771 (2000).
RN  [6]
RP  SEQUENCE FROM N.A.
RC  STRAIN=C57BL/6J; TISSUE=Spinal ganglion;
RA  Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA  Fukuda S., Furuno M., Hasegaki T., Hara A., Hashizume W.,
RA  Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA  Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA  Kato H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA  Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA  Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA  Saito K., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA  Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA  Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA  Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
RL  Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AK051454; BAC34647.1; -.
DR  MGD; MGI:1351327; Plazg7.
DR  GO; GO:0005615; C:extracellular space; TAS.
DR  GO; GO:0006954; P:inflammatory response; TAS.
DR  InterPro; IPR008262; Lipase AS.
DR  InterPro; IPR005065; PAF_Ac_hydrol_II.
DR  InterPro; IPR000379; Ser_estrs.
DR  Pfam; PF03403; PAF-AH_P_II; 1.
DR  PROSITE; PS00120; LIPASE_SER; 1.
DR  KMW; Glycoprotein; Hydrolase; Lipid degradation; Signal.
FT  CHAIN 1 21
FT  SIGNAL 21 436
FT  FT
FT  FT
FT  ACT_SITE 271 271
FT  ACT_SITE 294 294
FT  ACT_SITE 349 349
FT  CARBOHYD 76 76
FT  CARBOHYD 200 200
FT  CARBOHYD 324 324
SQ  SEQUENCE 436 AA; 49258 MW; 17C8B4D28F1ADC94 CRC64;

Query Match 69.4%; Score 633; DB 2; Length 440;
Best Local Similarity 70.2%; Pred. No. 9e-53;
Matches 120; Conservative 17; Mismatches 34; Indels 0; Gaps 0;

Qy 1 GHSPGGATVQTLSQDORFRCGIALDAWMPPLGDEVSRIPQPLFFINSEYFOYPAIIK 60
Db 270 GHSPGGATVQTLSQDORFRCGIALDAWMPPLGDEVSRIPQPLFFINSEYFOYPAIIK 329

Qy 61 MKKCYSPDKERKMITIRGSHVQNFADFTFATGKIIGHMLKLKGDIDSNAAIDLSNKASLA 120
Db 330 MKKCYSPDKERKMITIRGSHVQNFADFTFATGKIIGHMLKLKGDIDSNAAIDLSNKASLA 389

Qy 121 FLQHLGLHKDFQDQWCLIEGDDENLIPGNTINTNQHIMLQNSGIEKYN 171
Db 390 FLQHLGLHKDFQDQWCLIEGDDENLIPGSPFDVATVQPAQHSFGSQTON 440

RESULT 6
PAPA_CAVPO STANDARD; PRT; 436 AA.
AC P70683;
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Platelet-activating factor acetylhydrolase precursor (EC 3.1.1.47)
DE (PAF acetylhydrolase) (PAF 2-acylhydrolase) (LDL-associated
DE phospholipase A2) (LDL-PLA(2)) (2-acetyl-1-alkylglycerophosphocholine
DE esterase) (1-alkyl-2-acetyl-1-alkylglycerophosphocholine esterase).
GN Name=PLA2G7; Synonyms=PAFAH;
OC Cavia porcellus (Guinea pig);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

```

OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Hartley; TISSUE=Liver;
RX MEDLINE=97103479; PubMed=8947850;
RA Karasawa K., Kuge O., Kawasaki K., Nishijima M., Nakano Y., Tomita M.,
RA Yokoyama K., Sekita M., Nojima S.,
RT "Cloning, expression and characterization of plasma platelet-
RT activating factor-acetylhydrolase from guinea pig.";
RL J. Biochem. 120:838-844 (1996).
CC -I- FUNCTION: Modulates the action of platelet-activating factor (PAF)
CC by hydrolyzing the sn-2 ester bond to yield the biologically
CC inactive lyso-PAF. Has a specificity for substrates with a short
CC residue at the sn-2 position. It is inactive against long-chain
CC phospholipids.
CC -I- CATALYTIC ACTIVITY: 1-alkyl-2-acetyl-sn-glycero-3-phosphocholine +
CC H(2)O = 1-alkyl-sn-glycero-3-phosphocholine + acetate.
CC -I- SUBCELLULAR LOCATION: Extracellular.
CC -I- TISSUE SPECIFICITY: Plasma.
CC -I- SIMILARITY: Belongs to the AB hydrolase superfamily. Lipase
CC family.
CC
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CC or send an email to license@ebi.ac.uk).
CC
CC EMBL; D67037; BAA11054.1; -.
DR PIR; JC5021; JC5021.
DR InterPro; IPR008262; Lipase AS.
DR InterPro; IPR005065; PAF_Ac_hydrol_II.
DR InterPro; IPR000379; Ser_estrs.
DR Pfam; PF03403; PAF-AH_P_II; 1.
DR PROSITE; PS00120; LIPASE_SER; 1.
DR KMW; Glycoprotein; Hydrolase; Lipid degradation; Signal.
FT CHAIN 1 21
FT SIGNAL 21 436
FT  FT
FT  FT
FT  ACT_SITE 271 271
FT  ACT_SITE 294 294
FT  ACT_SITE 349 349
FT  CARBOHYD 76 76
FT  CARBOHYD 200 200
FT  CARBOHYD 324 324
SQ  SEQUENCE 436 AA; 49062 MW; C359D96E392FEE11 CRC64;

Query Match 68.8%; Score 627.5; DB 1; Length 436;
Best Local Similarity 70.8%; Pred. No. 2.7e-52;
Matches 121; Conservative 19; Mismatches 26; Indels 5; Gaps 1;

Qy 1 GHSPGGATVQTLSQDORFRCGIALDAWMPPLGDEVSRIPQPLFFINSEYFOYPAIIK 60
Db 269 GHSPGGATVQTLSQDORFRCGIALDAWMPPLGDEVSRIPQPLFFINSEYFOYPAIIK 328

Qy 61 MKKCYSPDKERKMITIRGSHVQNFADFTFATGKIIGHMLKLKGDIDSNAAIDLSNKASLA 120
Db 329 IEKPYQPKERKMITIRGSHVQNFADFTFATGKIIGHMLKLKGDIDSNAAIDLSNKASLA 388

Qy 121 FLQHLGLHKDFQDQWCLIEGDDENLIPGNTINTNQHIMLQNSGIEKYN 171
Db 389 FLQHLGLHKDFQDQWCLIEGDDENLIPGNTINTNQHIMLQNSGIEKYN 434

RESULT 7
PAPA_MOUSE STANDARD; PRT; 440 AA.
ID PAPA_MOUSE
AC Q60963;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)

```


Db 324 KKKLSSNDTKMTITKGSVHQSPDFTFFVSGELIGFFKLGKGEIDNEAIDCNHSL 383
Qy 120 AFLOKHLGLHKDFQDQWCLIEGDDENLIPGNTN 153
Db 384 AFLOKHLGLKDFQDQWCLIEGDDENLIPGNTN 417
RESULT 9
Q6NY17 PRELIMINARY; PRT; 404 AA.
AC Q6NY17;
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE Zgc:77563.
GN ORFNames=zgc:77563;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Udén T.B., Toshiki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX Strausberg R.;
RL EMBL; BC066578; AAH66578.1; -;
DR ZFIN; ZDB-GENE-040426-2248; zgc:77563.
DR GO; GO:0008247; C:2-acetyl-1-alkylglycerophosphocholine ester. ...; IEA.
DR GO; GO:0003847; F:1-alkyl-2-acetyl-glycerophosphocholine ester. ...; IEA.
DR GO; GO:0003844; P:1-alkyl-2-acetyl-glycerophosphocholine ester. ...; IEA.
DR GO; GO:0016042; P:lipid catabolism; IEA.
DR InterPro; IPR008262; Lipase AS.
DR InterPro; IPR005065; PAF Ac hydrolase II.
DR InterPro; IPR000379; Ser_estra.
DR Pfam; PF03403; PAF-AH_P_Ir; 1.
DR PROSITE; PS00120; LIPASE_SER; UNKNOWN 1.
SQ SEQUENCE 404 AA; 45743 MW; 2A2CEBFECE0828F CRC64;
Query Match 58.7%; Score 535; DB 2; Length 404;
Best Local Similarity 62.3%; Pred. No. 2.3e-43;
Matches 99; Conservative 27; Mismatches 33; Indels 0; Gaps 0;
Qy 1 GHSGGGATVIQTLSEDORFCGIALDAMWFLGDEVSRIPQLFFINSEYFQYFANI 60
Db 246 GHSGGGATVIECLCKEVRKCGVALDTWMPFLDEIPGVKQPIFFINSEKFWIGNIR 305
Qy 61 MKKCYSPDKRMKITIRGSHVQNFADFTTATGKTIHGLKULKGDIDSNAAIDLSNKASLA 120

Db 306 MKKLSAIFPRKMTITKGSVHQSPDFTFFVSGELIGFFKLGKGEIDPHIALDLCNKATLA 365
Qy 121 FLQKHLGLHKDFQDQWCLIEGDDENLIPGNTN 159
Db 366 FLQKHLGLKDFQDQWCLIEGDDENLIPGNTN 404
RESULT 10
PAF2 HUMAN STANDARD; PRT; 392 AA.
ID PAF2 HUMAN
AC Q99487; O15458;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Platelet-activating factor acetylhydrolase 2, cytoplasmic
(EC 3.1.1.47) (Serine dependent phospholipase A2) (HSD-PLA2).
GN Name=PAFAH2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
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RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=97115847; PubMed=8955149; DOI=10.1074/jbc.271.51.33032;
RA Hattori K., Adachi H., Matsuzawa A., Yamamoto K., Tsujimoto M.,
Aoki J., Hattori M., Arai H., Inoue K.;
RT "cDNA cloning and expression of intracellular platelet-activating
factor (PAF) acetylhydrolase II. Its homology with plasma PAF
acetylhydrolase.";
RL J. Biol. Chem. 271:33032-33038(1996).
RN [2]
RP SEQUENCE FROM N.A., SEQUENCE OF 1-5, AND MASS SPECTROMETRY.
RC TISSUE=Prostate;
RX MEDLINE=98161812; PubMed=9494101;
RA Rice S.Q.J., Southan C., Boyd H.F., Terrett J.A., Macphie C.H.,
Moore K., Gloger I.S., Tew D.G.;
RT "Expression, purification and characterization of a human serine-
dependent phospholipase A2 with high specificity for oxidized
phospholipids and platelet activating factor.";
RL Biochem. J. 330:1309-1315(1998).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Udén T.B., Toshiki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP REVIEW.
RX MEDLINE=97364701; PubMed=9218411; DOI=10.1074/jbc.272.29.17895;
RA Stafforini D.M., McIntyre T.M., Zimmerman G.A., Prescott S.M.;
RT "Platelet-activating factor acetylhydrolases.";
RL J. Biol. Chem. 272:17895-17898(1997).
CC -1- FUNCTION: Has a marked selectivity for phospholipids with short


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Query Match 36.7%; Score 335; DB 1; Length 392;
Best Local Similarity 44.4%; Pred. No. 5,7e-24;
Matches 67; Conservative 23; Mismatches 59; Indels 2; Gaps 1;

QY 1 GHSGGATVQTLSEDORECGIALDAMFPLGDEVYSRIPQPLFFINSEYFOYPANIIK 60
Db 234 GHSGGATVQTLSEDORECGIALDAMFPLGDEVYSRIPQPLFFINSEYFOYPANIIK 293
QY 61 MKKCYSPDKRKMITIRGSHQNFADFTFATGKIIGHMLK-LKGDIDSDNAADLSNKAS 118
Db 294 MKKICDQHQSRIITVLGSHVRSITDFVAGNWKSFSSHTRGSLDPYEGQETVVRAM 353
QY 119 LAFLOKHLGLHKDPQDWCCLIEGDENLIPG 149
Db 354 LAFLOKHLGLKEDYDQWNNFIEGIPSLTPG 384

RESULT 14
Q6GPX8 PRELIMINARY; PRT; 362 AA.
AC Q6GPX8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE MGC82533 protein.
GN Name=MGC82533;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
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RP SEQUENCE FROM N.A.
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madden A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RL initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RL initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RL prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RL prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]

DR GO; GO:0016042; P:lipid catabolism; IEA.
DR InterPro; IPR008262; Lipase AS.
DR InterPro; IPR005065; PAF AC hydrolase II.
DR InterPro; IPR000379; Ser_estr.
DR Pfam; PF03403; PAF-AH_D_II.1.
DR PROSITE; PS00120; LIPASE_SER; UNKNOWN 1.
SQ SEQUENCE 362 AA; 40280 MW; DAC93A288E9EB837 CRC64;

Query Match 33.8%; Score 308; DB 2; Length 362;
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Matches 60; Conservative 31; Mismatches 49; Indels 0; Gaps 0;

QY 1 GHSGGATVQTLSEDORECGIALDAMFPLGDEVYSRIPQPLFFINSEYFOYPANIIK 60
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Db 265 MKRLNAGNRESKAITILGSHVHSLSDSAFLSGFLADRILOPRAKLNPQCLOQTITSAUS 324
QY 121 FLQKHLGLHKDPQDWCCLIE 140
Db 325 FLQKHLGLPGNIPSLDSLSE 344

RESULT 15
Q9DB74 PRELIMINARY; PRT; 346 AA.
AC Q9DB74;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus adult male cerebellum cDNA, RIKEN full-length enriched
DE library, clone:1500005E13 product:phospholipase A2 group VII
DE [platelet-activating factor acetylhydrolase, plasma], full insert
DE sequences.
DE Names=Plazg7;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
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RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
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RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
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RL Nature 409:685-690(2001).
RN [3]
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RL Nature 409:685-690(2001).
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RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
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RL Nature 409:685-690(2001).
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RL Nature 409:685-690(2001).
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RN [3]
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RL Nature 409:685-690(2001).
RN [3]
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RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
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RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
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RL Nature 409:685-690(2001).
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RL Nature 409:685-690(2001).
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RL Nature 409:685-690(2001).
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RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
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RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK005158; BAB23849.1; -.
DR MGD; MGI:1351327; Pla2g7.
DR GO; GO:0005615; C:extracellular space; TAS.
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